

	L #	Hits	Search Text	DBs	Time Stamp
1	L1	5	arginine adj methyltransferase\$1	USPAT; US-PGPUB	2002/06/05 08:59
2	L2	1378	(steroid or glucocorticoid) adj receptor\$1	USPAT; US-PGPUB	2002/06/05 09:00
3	L3	5879	transcription\$ near6 (activat\$8 or coactivat\$8)	USPAT; US-PGPUB	2002/06/05 09:02
4	L4	217	(2 or 3) and methyltransferase\$1	USPAT; US-PGPUB	2002/06/05 09:03
5	L5	16	(2 or 3) same methyltransferase\$1	USPAT; US-PGPUB	2002/06/05 09:03
6	L6	20	1 or 5	USPAT; US-PGPUB	2002/06/05 09:03

PGPUB-DOCUMENT-NUMBER: 20020052308
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020052308 A1

TITLE: Nucleic acids, proteins and antibodies

PUBLICATION-DATE: May 2, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Rosen, Craig A.	Laytonsville	MD	US	
Ruben, Steven M.	Olney	MD	US	

US-CL-CURRENT: 514/1,435/183 ,435/320.1 ,435/325 ,435/6 ,435/69.1 ,435/7.1
,530/350 ,536/23.1

ABSTRACT:

This invention relates to newly identified tissue specific cancer associated polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "cancer antigens," and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such tissue specific cancer antigens for detection, prevention and treatment of tissue specific disorders, particularly the presense of cancer. This invention relates to the cancer antigens as well as vectors, host cells, antibodies directed to cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing tissue specific disorders, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.

DATE FILED: August 10, 2001

----- KWIC -----

BSTL:

109 784198 (AJ005893) JM26 [Homo sapiens] gnl.vertline.PID.vertline.e1289747
80 943 81 81 HNTNB85 Lung, >sp.vertline.O60828.vertline.O60828 JM26
PROTEIN, COMPLETE Pancreas, CDS (CLONE LLOXNC01U138D3 (BAYLOR Breast/
COLLEGE)). Length = 265 Ovarian 110 784868 WW-domain binding protein I [Mus
musculus] gi.vertline.1777577 1 969 77 85 HNTNQ08 Lung,
>sp.vertline.P97764.vertline.P97764 WW-DOMAIN BINDING Pancreas, PROTEIN 1.
Length = 305 Breast/ Ovarian 111 785428 translation initiation factor 5 [Homo
sapiens] gi.vertline.1229140 308 1606 87 87 HPMCI14 Lung,

>sp.vertline.P55010.vertline.IF5_HUMAN EUKARYOTIC Pancreas, TRANSLATION
 INITIATION FACTOR 5 (EIF-5). Breast/ Length = 431 Ovarian 112 785845 67 1350
 HCGBE06 Lung, Colon, Breast/ Ovarian 113 785854 3 509 HUSXJ65 Lung,
 Pancreas 114 786705 64 180 HBJJB89 Lung, Pancreas, Breast/ Ovarian 115
 787186 319 975 HUKBB89 Lung, Pancreas 116 787279 proteasome subunit z [Homo
 sapiens] gn.vertline.PID.vertline.d1007816 80 856 94 94 HKAJZ91 Lung,
 >sp.vertline.Q99436.vertline.Q99436 PROTEASOME SUBUNIT Z. Breast/ Length =
 277 Ovarian 117 789002 178 402 HATBM56 Lung, Pancreas, Breast/ Ovarian
 118 789008 1.8 kb mRNA (AA 1-84) [Homo sapiens] gi.vertline.33000 1354 1737
 100 100 HISCN20 Lung, >pir.vertline.S03384.vertline.S03384 hypothetical
 protein (IGF-II 3' Pancreas region) - human
 >sp.vertline.P09565.vertline.IG2- R_HUMAN PUTATIVE INSULIN-LIKE GROWTH
 FACTOR II ASSOCIATED PROTEIN. Length = 84 119 789555 (AL035247) hypothetical
 trp-asp repeat protein gn.vertline.PID.vertline.e1371207 124 1815 42 66
 HTTCB23 Pancreas, [Schizosaccharomyces pombe] Length = 760 Breast/ Ovarian
 120 789631 192 320 HLICN93 Lung, Pancreas, Colon 121 789779 1 396 HCHMS40
 Colon, Breast/ Ovarian 122 790387 3 527 HLMNA32 Colon, Breast/ Ovarian
 123 790461 (AF008445) phospholipid scramblase [Homo gi.vertline.2282601 105
 1193 99 99 HTGAV10 Lung, sapiens] >gnl.vertline.P1D.vertline.d1033532
 (AB006746) Pancreas, hMmTRA1b [Homo sapiens] >gi.vertline.4092081 Breast/
 (AF098642) phospholipid scramblase; plasma Ovarian membrane phospholipid
 scramblase [Homo sapiens] >sp.vertline.O15162.vertline.O15162 PHOSPHOLIPID
 SCRAMBLASE. >sp.vertline.G4 124 790931 2 394 HBCAO30 Pancreas, Breast/
 Ovarian 125 791176 (AB002107) hPer [Homo sapiens] >gi.vertline.2435507
 dbj.vertline. 3 1034 90 90 HNFCJ67 Lung, (AF022991) Rigui [Homo sapiens]
 AB002107_1 Pancreas >sp.vertline.O15534.vertline.O15534 RIGUI. Length =
 1290 126 791983 637 837 HBJLE45 Lung, Pancreas, Colon, Breast/ Ovarian
 127 792539 (AF020833) eukaryotic translation initiation factor 3
 gi.vertline.2460200 94 1068 94 94 HDPPX89 Lung, subunit [Homo sapiens]
 >sp.vertline.O14801.vertline.O14801 Pancreas, EUKARYOTIC TRANSLATION
 INITIATION Breast/ FACTOR 3 SUBUNIT. Length = 320 Ovarian 128 792749 protein
 arginine N-methyltransferase [Rattus gi.vertline.1390025 34 1104 95 96 HDQEP64
 Lung, norvegicus] >sp.vertline.Q63009.vertline.ANM1_RAT PROTEIN Breast/
 ARGININE N-METHYLTRANSFERASE 1 (EC Ovarian 2.1.1.-). Length = 353 129 792961
 (AF036249) polymerase I-transcript release factor; gi.vertline.2674195 778
 1305 85 86 HMEKG25 Lung, PTRF [Mus musculus] >sp.vertline.O54724.vert-
 line.O54724 Breast/ POLYMERASE I AND TRANSCRIPT RELEASE Ovarian FACTOR
 (POLYMERASE I-TRANSCRIPT RELEASE FACTOR). Length = 392 130 793206 dJ14O9.2
 (Melanoma-Associated Antigen MAGE gnl.vertline.PID.vertline.e1311294 889 1365
 99 99 HTWFN71 Lung, LIKE) [Homo sapiens]
 >sp.vertline.O76058.vertline.O7605- 8 Pancreas DJ14O9.2
 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE). Length = 606 131 793249
 proliferation associated gene (pag) gene product gi.vertline.287641 3 701 100
 100 HJAAE81 Lung, [Homo sapiens] >pir.vertline.A46711.vertline.A46711
 proliferation Pancreas, associated gene (pag) protein - human Length = 199
 Breast/ Ovarian 132 793626 alpha mannosidase II isozyme [Homo sapiens]
 gnl.vertline.PID.vertline.d1010153 119 640 99 99 HWABS13 Lung,
 >sp.vertline.P49641.vertline.MA2X_HUMAN ALPHA- Pancreas MANNOSIDASE IIX
 (EC 3.2.1.114) (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6- ALPHA-MANNOSIDASE) (MAN
 IIX). Length = 1139 133 794417 (AF047470) malate dehydrogenase precursor
 [Homo gi.vertline.2906146 3 1142 99 99 HFPBR03 Lung, sapiens]
 >sp.vertline.O43682.vertline.O436S2 MALATE Pancreas, DEHYDROGENASE (EC
 1.1.1.37) PRECURSOR Breast/ (EC 1.1.1.37). Length = 338 Ovarian 134 795197

82 888 HDPFT26 Lung, Breast/ Ovarian 135 795251 GAP SH3 binding protein
 [Homo sapiens] gi.vertline.1051170 101 1531 91 91 HE8FJ92 Pancreas,
 >sp.vertline.Q13283.vertline.Q13- 283 GAP SH3 BINDING Breast/ PROTEIN.
 Length = 466 Ovarian 136 795752 2 1018 HWBDR92 Lung, Pancreas 137 796261
 ubiquitin carrier protein E2 - human >gi.vertline.181916
 pir.vertline.B42856.vertline. 3 851 87 87 HCHPQ06 Colon, ubiquitin carrier
 protein [Homo sapiens] [SUB 23- B42856 Breast/ 247] Length = 247 Ovarian 138
 796933 lumican [Homo sapiens] Length = 338 gi.vertline.699577 49 1107 94 94
 HPMSD56 Lung, Pancreas, Prostate, Colon, Breast/ Ovarian 139 799424 525
 1553 HEONK47 Lung, Pancreas, Breast/ Ovarian 140 799698 1 426 HCHAM08
 Colon, Breast/ Ovarian 141 800351 DNAJ homolog [Homo sapiens]
 >gi.vertline.1127833 heat gi.vertline.1518918 282 860 83 84 HEMFP05
 Pancreas, shock protein hsp40 homolog [Homo sapiens] Breast/
 >pir.vertline.G02272.vertline.G02272 heat shock protein hsp40 Ovarian
 homolog - human >sp.vertline.Q13431.vertline.Q13431 HEAT SHOCK PROTEIN
 HSP40 HOMOLOG. Length = 178 142 800573 26S protease subunit [Sus scrofa]
 >gi.vertline.3193258 gn.vertline.PID.vertline.e235521 178 1383 93 93
 HCEVS28 Lung, (AF069053) proteasome subunit SUG1 [Bos taurus] Breast/
 >gnl.vertline.PID.vertline.d1012606 proteasomal ATPase (rat SUG1) Ovarian
 [Rattus norvegicus] >gnl.vertline.PID.vertline.d1023- 806 (AB000491)
 proteasome p45/SUG [Rattus norvegicus] >gnl.vertline.PID.vertline.e199326
 mSUG1 pr 143 805815 15 1055 HCHAP80 Lung, Colon, Breast/ Ovarian 144
 806445 711 1028 HTELC67 Lung, Pancreas 145 810309 (AF098482) transcriptional
 coactivator

PGPUB-DOCUMENT-NUMBER: 20020052014
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020052014 A1

TITLE: Protein methylarginine-specific antibodies

PUBLICATION-DATE: May 2, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Aletta, John M.	Williamsville	NY	US	

US-CL-CURRENT: 435/7.92,530/330 ,530/387.9

ABSTRACT:

The present invention provides antisera that specifically recognize peptides containing methylated arginines. The present invention also provides peptides for producing the antisera. Also provided is a method for the detection of methylation status of proteins and peptides, and compositions that affect the methylation status.

DATE FILED: December 21, 2000

----- KWIC -----

BSTX:

[0005] The enzymes responsible for protein methylation, protein arginine methyl transferases (PRMT) are currently classified into two distinct categories. One type of activity (Type I) produces asymmetric dimethylation of the n.sub.1 terminal guanidino nitrogen of arginines in substrate proteins, particularly glycine- and arginine-rich (GAR) segments of proteins. Proteins that are substrates for this reaction include nucleolin, fibrillarin, and several hnRNPs. Type II arginine methyltransferase activity produces symmetric dimethylation of both terminal nitrogens of specific protein arginines. Myelin basic protein is a recognized substrate for this activity.

DETX:

[0034] In this embodiment, the antisera of the present invention was used to determine methylation status of proteins in vitro. To illustrate this embodiment, the RNA binding protein from T.brucei (RBP16) was expressed as a fusion with maltose binding protein (MBP-RBP16). The fusion protein has a mass of 55 kDa. The recombinant protein from T.brucei contains 5 GRG repeats. The ability of the antisera of the present invention to detect methylated form of this protein was determined by using crude cell extracts as a source of the enzyme protein arginine methyltransferase. To achieve methylation, 1 .mu.g of MBP-RBP16 was incubated in Tris buffer (pH 8.0) containing 100 .mu.M

S-adenosylmethionine (SAM) and no extract (-), 10 .mu.g of a PC12 cell nuclear extract (PC12), 100 .mu.g of a whole cell extract of T.brucei (WC) or 50 .mu.g of a T.brucei mitochondrial extract (mitos). The reaction tube contents were separated on a 10% SDS PAGE gel and transferred to PVDF membrane. The membrane was incubated with 1:1000 dilution of the anti-mRG serum and .sup.125I-labeled anti-rabbit secondary antibody was used to detect the binding of the primary anti-mRG antiserum by autoradiography. As shown in FIG. 2, no detectable signal is observed in the lane without any extract. A 2.5 fold increased signal is observed in the lane containing PC12 extract while T.brucei WC and mitos extracts increased the signal by 10.6 and 17.9 fold respectively. These results demonstrate that the antibodies of the present invention can be used to identify methylation of proteins in vitro.

PGPUB-DOCUMENT-NUMBER: 20020045158
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020045158 A1

TITLE: Cells for drug discovery

PUBLICATION-DATE: April 18, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Case, Casey	San Mateo	CA	US	

US-CL-CURRENT: 435/4,435/325

ABSTRACT:

Disclosed herein are compositions and method useful in screening a compound for its interaction and/or effect with a molecular target and/or cellular process.

DATE FILED: February 8, 2001

----- KWIC -----

DETX:

[0084] Common regulatory domains for addition to the zinc finger protein include, e.g., effector domains from transcription factors (activators, repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos and/or erb family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., methyltransferases, topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20020040489
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020040489 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: April 4, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gorlach, Jom	Durham	NC	US	
An, Yong-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Raines, Tracy M.	Durham	NC	US	
Yu, Yang	Martinsville	NJ	US	
Rameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Ledford, Brooke L.	Holly Springs	NC	US	
Woessner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Kricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US-CL-CURRENT: 800/288,435/4 ,536/23.2 ,536/23.6

ABSTRACT:

Isolated nucleotide compositions and sequences are provided for Arabidopsis thaliana genes. The nucleic acid compositions find use in identifying homologous or related genes; in producing compositions that modulate the expression or function of its encoded protein, mapping functional regions of the protein; and in studying associated physiological pathways. The genetic sequences may also be used for the genetic manipulation of cells, particularly of plant cells. The encoded gene products and modified organisms are useful for screening of biologically active agents, e.g. fungicides, insecticides, etc.; for elucidating biochemical pathways; and the like.

DATE FILED: January 26, 2001

----- KWIC -----

DET L:

75 2025075 Tyr_Phospho_Site(42-49) 76 2025076 4E-90 > dbj.vertline.BAA78331.1.vertline. (AB014076) histidine decarboxylase [Brassica napus] Length = 490 77 2025077 3E-22 > pir.vertline..vertline.A30191 hypothetical protein L - Bacillus subtilis (fragment) Length = 171 78 2025078 9E-33 > sp.vertline.O23760.vertline.COMT_CLABR CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) > gi.vertline.2240207 (AF006009) caffeic acid O-methyltransferase [Clarkia breweri] Length = 370 79 2025079 2E-55 > sp.vertline.O64765.vertline.U- AP1_ARATH PROBABLE UDP-N- ACETYLGLUCOSAMINE PYROPHOSPHORYLASE > gi.vertline.3033397 (AC004238) unknown protien [Arabidopsis thaliana] Length = 502 80 2025080 7E-27 > gb.vertline.AAD46402.1.vertline.AF096246_1 (AF096246) ethylene-responsive transcriptional coactivator [Lycopersicon esculentum] Length = 146 81 2025081 Tyr_Phospho_Site(102-110) 82 2025082 Rgd(1288-1290) 83 2025083 Pkc_Phospho_Site(10-12) 84 2025084 1E-79 > emb.vertline.CAB36755.1.vertline. (AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana] Length = 258 85 2025085 7E-47 > gi.vertline.2078350 (U95923) transaldolase [Solanum tuberosum] Length = 438 86 2025086 Tyr_Phospho_Site(2057-2063) 87 2025087 Pkc_Phospho_Site(77-79) 88 2025088 0 > sp.vertline.P43296.vert- line.RD19_ARATH CYSTEINE PROTEINASE RD19A PRECURSOR > gi.vertline.541856.vertline.pir.vertline..vertline.JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana > gi.vertline.435618.vertline.dbj.ver- tline.BAA02373.vertline. (D13042) thiol protease [Arabidopsis thaliana] > gi.vertline.4539328.vertline.emb.vertline.CAB38829.1.vertl- ine. (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana] Length = 368 89 2025089 3E-98 > emb.vertline.CAA92583.vertline. (Z68291) cysteine protease [Pisum sativum] Length = 350 90 2025090 8E-88 > gi.vertline.1245182 (U49398) sterol delta-7 reductase [Arabidopsis thaliana] Length = 430 91 2025091 Tyr_Phospho_Site(1016-1023) 92 2025092 9E-14 > gi.vertline.4097547 (U64906) ATRP3 [Arabidopsis thaliana] Length = 297 93 2025093 1E-115 > gi.vertline.3785999 (AC005499) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] Length = 199 94 2025094 Tyr_Phospho_Site(328-334) 95 2025095 4E-46 > sp.vertline.Q42614.vertline.NLT1_BRANA NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) > gi.vertline.732520 (U22105) germination-specific lipid transfer protein 1 [Brassica napus] Length = 117 96 2025096 Tyr_Phospho_Site(512-519) 97 2025097 Tyr_Phospho_Site(781-789) 98 2025098 1E-102 > emb.vertline.CAA04707.vertline. (AJ001374) alpha-glucosidase [Solanum tuberosum] Length = 919 99 2025099 Pkc_Phospho_Site(320-322) 100 2025100 Zinc_Protease(861-870) 101 2025101 Tyr_Phospho_Site(592-600) 102 2025102 1E-29 > embICAAL5099I(AJ235272) SOS RIBOSOMAL PROTEIN L3 103 2025103 3' Pkc_Phospho_Site(38-40) 104 2025104 5' Pkc Phos ho Site 18-20 105 2025105 4E-59 > pir11560129 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]>gi.vertline.926933 (L 106 2025106 1E-116) > spIP46643IAATL.ARATH ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) > gi.vertline.693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana]>9113201622 (AC004669) aspartate aminotransferase [Arabido 107 2025107 3E-61) > gblAAD5S28S.11AC00826396 (AC008263) Similar to gblAF135422 GDP-mannose pyrophosphorylase A (GMPPA) from Homo sapiens. ESTs gblAA7I 2990, gblN65247,

gb|N38| 49, gb|vertline.T041 79, gb|Z38092, gb|T76473, gb|N96403, gb|AA394551
 and gb| 108 2025108 6E-72 >sp|P55737|HS82_ARATH HEAT SHOCK PROTEIN 81-2
 (HSP81-2) >gi|445127|jprf.vertline.j1908431B heat shock protein HSP81-2
 [Arabidopsis thaliana] Length = 699 109 2025109 Rgd(531-533) 110 2025110
 3E-39 >pir11539445 DNA-directed RNA polymerase (EC 2.7.7.6)11 chain 9 -
 fruit fly (*Drosophila melanogaster*) >gi|4S3OI 1 lbbsl 39686 (S66940) RNA
 polymerase II subunit 9, RPII15 B9 [EC 2.7.7.6][*Drosophila melanogaster*,
 Peptide, 129 aa][*Drosophila melanogaster*]Length 129 111 2025111 2E-51
 >emblCABSO787.11 (AJ243528) glyoxalase I [*Triticum aestivum*] Length = 284
 112 2025112 PtsHprSer(1091-1106) 113 2025113 1 E-106 >gi.vertline.3128188
 (AC004521) beta-glucosidase [Arabidopsis thaliana]Length 577 114 2025114
 4E-93 >g.vertline.j3738327 (AC005170) serine carboxypeptidase [Arabidopsis
 thaliana]Length = 474 115 2025115 Tyr_Phospho_Site(51 8-524) 116 2025116
 4E-70 >gb|AADS0011.1|AC007651fi (AC007651) Similar to translation
 initiation factor 1F2 [Arabidopsis thaliana]Length = 1016 117 2025117 1
 E-17 >sp|P41 73411|AH1_YEAST ISOAMYL ACETATE-HYDROLYZING ESTERASE
 >91110771 851pir1154991 1 hypothetical protein YORI 26c - yeast
 (*Saccharomyces cerevisiae*) >g.vertline.l600023|emb ICAA581 041 (X82930) ORE
Saccharomyces cerevisiae >g.vertline.11050 118 2025118 3'
 Tyr_Phospho_Site(523-530) 119 2025119 5' Rgd(1053-1055) 120 2025120 2E-52
 >emblCAA07S66I (AJ007578) pRIBS protein Ribes nigrum Length = 2S8 121
 2025121 5E-96 >gi.vertline.2708813 (AF037362) ATA2O [Arabidopsis
 thaliana]Length 432 122 2025122 1 E-63 >emb CAB 10269.11 (Z97337)
 hydroxyprol me-rich glycoprotein homolog [Arabidopsis thaliana]Length = 507
 123 2025123 Tyr_Phospho_Site(1 3-20) 124 2025124 4E-24 >emblCAA74S911
 (Y14199) MAP3K delta-i protein kinase [Arabidopsis thaliana]Length = 406 125
 2025125 IE-14 >gi.vertline.308906 (L18909) thioredoxin [*Lilium*
longiflorum]Length = 262 126 2025126 Tyr_Phospho_Site(60-68) 127 2025127
 IE-iLO) >embfCAA06978.11 (AJ006309) protein tyrosine phosphatase Arabido
 sis thaliana Len th = 340 128 2025128 6E-50 >emblCAA7OS78I(Y09427)
 squamosa-promoter binding protein like 3 [Arabidopsis
 thaliana]>g.vertline.5931 6511emblCAB56579.11 (AJOI 1627) squamosa promoter
 binding protein-like 3 [Arabidopsis thaliana]
 >gi.vertline.59316631emb10AB56585.1 (AJ01 1633) squamosa promoter binding
 protein- like 3 [Arabidopsis thaliana]Length = 131 129 2025129 4E-47
 >gi.vertline.2708813 (AF037362) ATA2O [Arabidopsis thaliana]Length = 432
 130 2025130 Tyr_Phospho_Site(88-96) 131 2025131 3' Protein Splicing(530-537)
 132 2025132 3' Tyr_Phospho_Site(504-512) 133 2025133 3E-23
 >gb.vertline.AAD55621 .1 IACOO8OI 631 (ACOO8O1 6) Is a member of PF100534
 Glycosyl transferases group 1. EST gb.vertline.N967O2

PGPUB-DOCUMENT-NUMBER: 20020023280
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020023280 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: February 21, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gorlach, Jom	Durham	NC	US	
An, Yong-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Raines, Tracy M.	Durham	NC	US	
Yu, Yang	Martinsville	NJ	US	
Rameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Ledford, Brooke L.	Holly Springs	NC	US	
Woessner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Kricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US-CL-CURRENT: 800/288,435/4 ,536/23.2 ,536/23.6

ABSTRACT:

Isolated nucleotide compositions and sequences are provided for Arabidopsis thaliana genes. The nucleic acid compositions find use in identifying homologous or related genes; in producing compositions that modulate the expression or function of its encoded protein, mapping functional regions of the protein; and in studying associated physiological pathways. The genetic sequences may also be used for the genetic manipulation of cells, particularly of plant cells. The encoded gene products and modified organisms are useful for screening of biologically active agents, e.g. fungicides, insecticides, etc.; for elucidating biochemical pathways; and the like.

DATE FILED: January 26, 2001

----- KWIC -----

DETL:

274 508 2027508 Tyr_Phospho_Site(733-741) 509 2027509 6E-81)
 >gi.vertline.2832241 (AF030864) nonphototropic hypocotyl 1 [Arabidopsis thaliana] Length = 996 510 2027510 6E-82
 >gb.vertline.AAD26977.1.vertline.AC007265_2 (AC007265) unknown protein [Arabidopsis thaliana] Length = 283 511 2027511 3' 1E-18
 >gi.vertline.2252840 (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]
 >gi.vertline.6049882.vertline.gb.vertline.AAF02797.1.vertline.AF- 195115_17 (AF195115) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] Length = 746 512 2027512 3' Tyr_Phospho_Site(740-746) 513 2027513 3' Tyr_Phospho_Site(837-844) 514 2027514 5' 1E-52
 >gi.vertline.5302805.vertline.emb.vertline.CAB46046.1.vertline. (Z97342) disease resistance RPP5 like protein [Arabidopsis thaliana] Length = 1304 515 2027515 5' 3E-54
 >gi.vertline.2245037.vertline.emb.vertline.CAB10456.1.vertline. (Z97342) nuclear antigen homolog [Arabidopsis thaliana] Length = 355 516 2027516 5' 1E-81 >gi.vertline.4455342.vertline.emb.vertline.CAB36723.vertline. (AL035522) O-methyltransferase-like protein [Arabidopsis thaliana] Length = 382 517 2027517 5' 1E-89 >gi.vertline.1363489.vertline.pir.parallel.S57621 thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi.vertline.984052.vertline.emb.vertline.CAA61592.vertline. (X89413) thioglucoside glucosylhydrolase [Arabidopsis thaliana] >gi.vertline.5524767.vertline.emb.vertline.CAB50792.1.vertline. (AJ243490) thioglucoside glucosylhydrolase [Arabidopsis thaliana] Length = 524 518 2027518 5' Pkc_Phospho_Site(68-70) 519 2027519 5' Tyr_Phospho_Site(689-695) 520 2027520 5' Wd_Repeats(856-870) 521 2027521 5' Tyr_Phospho_Site(332-339) 522 2027522 3E-50 >gi.vertline.2191159 (AF007270) Similar to serine hydroxymethyltransferase; coded for by A. thaliana cDNA T42313; coded for by A. thaliana cDNA W43384 [Arabidopsis thaliana] Length = 532 523 2027523 2E-40 >sp.vertline.O22048.vertline.AX1- C_ARATH ALTERNATIVE OXIDASE 1C PRECURSOR >gi.vertline.2506049.- vertline.dbj.vertline.BAA22635.vertline. (AB003175) alternative oxidase [Arabidopsis thaliana] Length = 329 524 2027524 Tyr_Phospho_Site(277-285) 525 2027525 Tyr_Phospho_Site(634-641) 526 2027526 Pkc_Phospho_Site(12-14) 527 2027527 Tyr_Phospho_Site(461-469) 528 2027528 1E-75 >dbj.vertline.BAA37167.vertline. (AB008097) cytochrome P450 [Arabidopsis thaliana] Length = 524 529 2027529 2E-85 >dbj.vertline.BAA36337.vertline. (AB015143) AHP3 [Arabidopsis thaliana] Length = 155 530 2027530 1E-16 >pir.parallel.S30515 wound-induced protein -western balsam poplar >gi.vertline.20956.vertline.emb.vertline.CAA39082.vertline. (X55440) unnamed protein product [Populus balsamifera subsp. trichocarpa] >gi.vertline.20965.vertline.emb.vertline.CAA40072.vertline. (X56752) unnamed protein product 531 2027531 1E-50 >sp.vertline.P49967.vertline.SR53_ARATH SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 3 (SRP54) >gi.vertline.515681 (U12127) signal recognition particle 54 kDa subunit [Arabidopsis thaliana] Length = 495 532 2027532 1E-27 >gb.vertline.AAC50037.1.vertline. (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana] Length = 765 533 2027533 7E-34 >sp.vertline.P48496.vertline.TPIC_SPIOL TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)

>gi.vertline.1084309.vertline.pir.parallel.S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi.vertline.806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea] Length = 322 534 2027534 3' 4E-18
 >gi.vertline.4836892.vertline.gb.vertline.AAD3059- 5.1.vertline.AC007369_5 (AC007369) RNA helicase [Arabidopsis thaliana] Length = 2171 535 2027535 3' Pkc_Phospho_Site(2-4) 536 2027536 3' Pkc_Phospho_Site(2-4) 537 2027537 3' 1E-20
 >gi.vertline.4827050.vertline.ref.vertline.NP_005142.1.vertline.pUSP14- .vertline. ubiquitin specific protease 14 (tRNA-guanine transglycosylase)
 >gi.vertline.1729927.vertline.sp.vertline.P54578.ver- tline.TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi.vertline.940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens] Length = 494 538 2027538 3' 8E-44
 >gi.vertline.4240116.vertline.dbj.vert- line.BAA74837.vertline. (AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana]
 >gi.vertline.4240118.vertline.dbj.vertline.BAA7- 4838.vertline. (AB007800) NADH- cytochrome b5 reductase [Arabidopsis thaliana] Length = 281 539 2027539 3' Tyr_Phospho_Site(123-131) 540 2027540 3' Pkc_Phospho_Site(30-32) 541 2027541 5' Pkc_Phospho_Site(67-69) 542 2027542 5' 2E-33
 >gi.vertline.4469408.vertline.gb.vertline.AAD21248.vertline. (AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana]
 >gi.vertline.4469410.vertline.gb.vertline.AAD21249.vertline. (AF116528) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana] Length = 196 543 2027543 5' Rgd(488-490) 544 2027544 5' 4E-14
 >gi.vertline.728867.vertline.sp.vertline.P40602.v- ertline.APG_ARATH ANTER-SPECIFIC PROLINE- RICH PROTEIN APG PRECURSOR
 >gi.vertline.99694.vertline.pir.parallel.S21961 proline-rich protein APG - Arabidopsis thaliana >gi.vertline.22599.vertlin- e.emb.vertline.CAA42925.vertline. (X60377) APG [Arabidopsis thaliana] Length = 534 545 2027545 4E-16 >emb.vertline.CAB57788- .1.vertline. (AJ250130) transcripton factor [Anabaena PCC7120] Length = 319 546 2027546 1E-73
 >sp.vertline.P42801.vertline.INO- 1_ARATH MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi.vertline.1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana] Length = 511 547 2027547
 Pkc_Phospho_Site(8-10) 548 2027548 Pkc_Phospho_Site(91-93) 549 2027549 Tyr_Phospho_Site(960-968) 550 2027550 3E-95
 >gb.vertline.AAD25756.1.vertline.AC007060_14 (AC007060) Contains the PF.vertline.00650 CRAL.vertline.TRIO phosphatidyl-inositol-trans- fer protein domain. ESTs gb.vertline.T76582, gb.vertline.N06574 and gb.vertline.Z25700 come from this gene. [Arabidopsis thaliana] Length = 540 551 2027551
 Pkc_Phospho_Site(153-155) 552 2027552 Tyr_Phospho_Site(11-19) 553 2027553 4E-15 >sp.vertline.Q03251.vertline.GRP8_ARATH GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi.vertline.419756.vertline.pir.par- allel.S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana
 >gi.vertline.16305.vertline.emb.vertline.CAA78712.vertline. (Z14988) glycine rich protein [Arabidopsis thaliana] >gi.vertline.166658 (L04171) ORF [Arabidopsis thaliana] >gi.vertline.166839 (L00649) RNA-binding protein [Arabidopsis thaliana]
 >gi.vertline.4914438.vertline.emb.vertline.CAB43641- .1.vertline. (AL050351) glycine-rich protein (clone AtGRP8) [Arabidopsis thaliana] Length = 169 554 2027554 1E-89 >gb.vertline.AAF00632.1.vertline.AC009540_9

(AC009540) unknown protein [Arabidopsis thaliana] Length = 318 555 2027555
 4E-84 >gi.vertline.4220474 (AC006069) myosin heavy chain [Arabidopsis
 thaliana] Length = 629 556 2027556 Tyr_Phospho_Site(593-599) 557 2027557
 2E-52 >sp.vertline.P93568.vertline.UGS2_SOLTU SOLUBLE GLYCOGEN [STARCH]
 SYNTHASE PRECURSOR (SS I)
 >gi.vertline.1781353.vertline.emb.vertline.CAA71442.vertline. (Y10416)
 soluble starch (bacterial glycogen) synthase [Solanum tuberosum] Length = 641
 558 2027558 Pkc_Phospho_Site(53-55) 559 2027559 3E-16 >gi.vertline.3170570
 (AF058302) FmE [Streptomyces roseofulvus] Length = 216 560 2027560
 Pkc_Phospho_Site(45-47) 561 2027561 Tyr_Phospho_Site(62-70) 562 2027562 1E-17
 >gi.vertline.3152569 (AC002986) Contains similarity to YELA protein
 gb.vertline.U63062 from Dictyostelium discoideum. [Arabidopsis thaliana]
 Length = 396 563 2027563 Tyr_Phospho_Site(559-566) 564 2027564
 Pkc_Phospho_Site(35-37) 565 2027565 3' Tyr_Phospho_Site(848-855) 566 2027566
 3' 1E-28
 >gi.vertline.116229.vertline.sp.vertline.P29197.vertline.CH60_ARATH
 CHAPERONIN CPN60, MITOCHONDRIAL PRECURSOR (HSP60)
 >gi.vertline.99676.vertline.pir.parallel.S20876 chaperonin hsp60 precursor
 - Arabidopsis thaliana >gi.vertline.16221.vertline.emb-
 .vertline.CAA77646.vertline. (Z11547) chaperonin hsp60 [Arabidopsis thaliana]
 Length = 577 567 2027567 3' Tyr_Phospho_Site(166-172) 568 2027568 3'
 Tyr_Phospho_Site(837-844) 569 2027569 3' 2E-35
 >gi.vertline.6324622.vertline.ref.vertline-
 .NP_014691.1.vertline.RAT1.vertline. RNA trafficking protein; transcription
 activator; Rat1p >gi.vertline.417592.vertline.sp.vertlin-
 e.Q02792.vertline.RAT1_YEAST RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3'
 EXORIBONUCLEASE) (P116) >gi.vertline.83014.vertline.- pir.parallel.S20126
 exoribonuclease RAT1 (EC 3.1.11.-) - yeast (Saccharomyces cerevisiae) >
 570 2027570 5' 2E-15
 >gi.vertline.6358556.vertline.gb.vertline.AAF07233.1.vertline. (AF146842)
 cyc1A protein [Antirrhinum graniticum]
 >gi.vertline.6358558.vertline.gb.vertline.AAF07235.1.vertline. (AF146844)
 cyc1A protein [Antirrhinum molle] Length = 270 571 2027571 5' 6E-70
 >gi.vertline.1399267 (U31752) calmodulin-domain protein kinase CDPK
 isoform 4 [Arabidopsis thaliana]
 >gi.vertline.5916441.vertline.gb.vertline.AAD55952.1.vertline.AC007633- _1
 (AC007633) calmodulin-domain protein kinase CDPK isoform 4 (CPK4)
 [Arabidopsis thaliana] Length = 501

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ABSTRACT:

Human stress arrays and methods for their use are provided. The subject arrays include a plurality of polynucleotide spots, each of which is made up of a polynucleotide probe composition of unique polynucleotides corresponding to a human stress gene. The subject arrays find use in hybridization assays, particularly in assays for the identification of differential gene expression of human stress genes.

DATE FILED: February 13, 2001

----- KWIC -----

DETL:

(APAF1) AF013263 Q14727 CA034 DNA recombination & repair protein HNGS1
AF022778 Q43475 mitogen-activated protein kinase kinase 7 (MAP kinase kinase
7; MAPKK7; MAP2K7; PRKMK7); MAPK/ERK kinase 7 (MEK7); c-jun N-terminal CA035
kinase kinase 2 (JNKK2) AF022805 Q14816; Q60452 cysteine-rich anigogenic
inducer 61 (CYR61); insulin-like growth factor-binding protein 10 (IGE-
CA043 binding protein 10; IGFBP10); GIG1 AF031385 Q00622; Q14934
cAMP-responsive element modulator 1 alpha CA053 protein (HCREM) D14825 Q14501
MCM2 DNA replication licensing factor; nuclear CA057 protein BM28; KIAA0030
D21063 P49736 CA062 KIAA0078 D38551 Q60216 P02593; P99014; P70667; Q61379;
CA066 calmodulin (CALM; CAM) D45887 Q61380 CA070 cysteine protease 055696
Q99538 CA087 fibroblast adenine nucleotide translocator 2 (ANT2) J02683
P05141; O43350 CA090 uroporphyrinogen III synthase J03824 P10746 CA093
leukocyte IgG Fo receptor (FCGR) J04162 P08637 CA103 interferon-gamma IEE SSP
5111 L07633 Q06323 CA111 aryl hydrocarbon receptor (AH receptor) L19872
P35869 CA119 glutathione S-transferase theta 2 (GSTT2) L38503 P30712 CA121
protein phosphatase 2A B56-alpha L42373 Q15172 CA122 protein phosphatase 2A
B56-beta (PP2A) L42374 Q15173 protein phosphatase PP2A 61-kDa regulatory
CA124 subunit epsilon L76703 Q16537 signal transducer and activator of

transcription 4 CA125 (STAT4) L78440 Q14765 eukaryotic translation
initiation factor 4E 25-kDa CA127 subunit (EIF4E); mRNA cap-binding protein
M15353 P06730 2-oxoisovalerate dehydrogenase alpha subunit; branched-chain
alpha-keto acid dehydrogenase CA131 component alpha subunit (BCKDH EI-alpha)
M22221 P12694 CA134 elk-1; ets-related proto-oncogene M25269 P19419 CA143
GTP-binding nuclear protein RAN (TC4) M31469 P17080 cAMP-dependent protein
kinase beta catalytic CA152 subunit (PKAC-beta; PRKACB) M34181 P22694
cAMP-dependent protein kinase gamma-catalytic CA153 subunit (PKA C-gamma)
M34182 P22612 CA160 deoxycytidine kinase M60527 P27707 CA167 complement
component 5 (CS) M65134 P01031 CA175 lymphocyte antigen M81141 Q30099
interleukin 16 (IL16); lymphocyte chemoattractant CA181 factor (LCF) M90391
Q14005 serine/threonine protein phosphatase 2B catalytic subunit gamma;
calmodulin-dependent calcineurin A subunit gamma; testis-specific calcineurin
CA186 catalytic subunit (CAM-PRP catalytic subunit) S46622 P48454 CA197
serine/threonine protein kinase U07358 Q12852 serine/threonine-protein kinase
NEK2; NI MA- related protein kinase 2; NIMA-like protein kinase 1; CA204
HSPK21 U11050 P51955 CA206 40S ribosomal protein S5 (RPS5) U14970 P46782
CA226 58-kDa inhibitor of the RNA-activated protein kinase U28424 Q13217
CA229 interleukin 15 receptor alpha subunit U31628 Q13261 CA230 histone
deacetylase 2 (HD2) U31814 Q92769 CA234 TAXI-binding protein 151 (TXBP151)
U33821 Q13311 glutathione synthetase (GSH synthetase; GSH-S); CA237
glutathione synthase U34683 P48637 CA242 xanthine dehydrogenase/oxidase U39487
P47989 mothers against decapentaplegic homolog 4 CA251 (DPC4; MADH4; SMAD4)
U44378 Q13485 CA255 CREB-binding protein U47741 Q92793 CA263 hint protein;
protein kinase C inhibitor 1 (PKCI1) U51004 P49773 CA271 serine/threonine
protein kinase KRS2 U60207 Q15802 CA276 preferentially expressed antigen of
melanoma U65011 P78395 CA277 mitotic feedback control protein MADP2 homolog
U65410 Q13257 branched-chain amino acid aminotransferase CA281 mitochondrial
(BCAT(M)) U68418 O15382 CA290 HSIH2 U76248 O43270 CA294 TSG101 tumor
susceptibility protein U82130 Q99816 maleylacetoacetate isomerase (MAA1);
glutathione CA299 transferase zeta 1 U86529 O43708 autoimmune antigen
cancer/testis antigen NY-ESO-1; CA300 LAG E-1 U87459 P78358 purine
nucleoside phosphorylase (PNP); inosine CA308 phosphorylase X00737 P00491
CA313 cathepsin L; major excreted protein (MEP) X12451 P07711 regulator of
chromosome condensation; cell cycle CA314 regulatory protein X12654 P18754
ribonucleoside-diphosphate reductase M1 subunit; CA328 ribonucleotide
reductase X59543 P23921 CMP-N-acetylneuraminic acid-beta-galactosamide-
alpha-2,6-sialyltransferase; beta-galactoside alpha- 2,6-sialyltransferase
(alpha-2,6-ST); CA331 sialyltransferase 1 (SIAT1); B-cell CD75 antigen X62822
P15907 DNA primase small subunit; DNA primase 49-kDa CA340 subunit X74330
P49642 minichromosome maintenance deficient homolog 4 CA341 (MCM4); CDC21
homolog; CDC54 homolog X74794 P33991; Q99658 CA350 thioredoxin reductase
X91247 Q16881 CA355 serine/threonine protein kinase X97630 Q15524
secretogranin 1 (SGI; SOG1); chromogranin B CA358 (CHGB) Y00064 P05060 ets
domain protein elk-3; NET; SRF accessory CA379 protein 2 (SAP2) Z36715 P41970
alpha-N-acetylneuraminic acid alpha-2,8- sialyltransferase; ganglioside GD3/GT3
synthase; CA386 sialyltransferase 8 (SIAT8) L32867 Q92185 glutamate-cysteine
ligase regulatory subunit CA387 (GLCLR); gamma-glutamylcysteine synthetase
L35546 P48507 estrogen receptor 1 (ESR1); estrogen receptor alpha (ER-alpha;
ESRA); fatty acid M12674; X03635; P03372; Q14276; CA389 synthase/estrogen
receptor fusion protein (FAS/ER) U47678; AF172068 Q13511 soluble
galactose-binding lectin 3 (LGALS3); LGALS2; galectin 3, macrophage
galactose-specific lectin 2 (MAC2); galactoside-binding protein CA394

(GALBP) M35368 P17931; Q16005 CA397 LOX (Protein-lysine 6-oxidase, Lysyl-Oxidase) M94054 P28300 CA401 stanniocalcin (STC) U25997 P52823 RAD51 B, RAD51 LI, REC2, R51 H2 (DNA repair CA406 protein RAD 51 Homolog 2) U92074 O60914; O15315 CA407 SAP18 (Sin3 associated polypeptide P18) U96915 Q00422 CA414 RAD51C truncated protein AF029670 Q43503 chromodomain-helicase-DNA-binding protein 1 CA419 (CHD1) AF006513 Q14646 CA420 CDC7-related kinase AF015592 Q00311 stratifin (SFN); 14-3-3 protein sigma; epithelial cell CA426 marker protein 1; HMEI AF029082 P31947 CA431 testis-specific protein kinase 1 D50863 Q15569 CA438 KIAA0204 D86959 Q92603 CA444 microtubule-associated protein 1B L06237 P46821 CA445 Von Hippel-Lindau tumor suppressor protein (VHL) L15409 P40337 CA446 thymidylate kinase L16991 P23919 A-raf proto-oncogene serine/threonine-protein CA450 kinase; PKS2 L24038 P10398 importin beta 1 subunit; karyopherin beta 1 subunit; CA452 importin 90; nuclear factor p97 L38951 Q14974 (2'-5')oligoadenylate synthetase 1 ((2'-5')oligo(A) CA459 synthetase 1; 2-5A synthetase 1) M11810 P00973 eukaryotic translation initiation factor 2 alpha CA482 subunit (EIF2-alpha) U26032 none CA487 betaine-homocysteine S-methyltransferase U50929 Q93088 CA488 mitogen-responsive phosphoprotein DOC2 U53446 Q13598 CA498 MYD88 U70451 P78397 CA502 microsomal glutathione S-transferase 2 (MGST2) U77604 Q99735 transcription factor activating enhancer-binding CA506 protein 2 gamma (AP2-gamma; TFAP2C) U85658 Q92754 CA508 serine kinase SRPK2 U88666 P78362 CA510 growth-arrest-specific protein 2 (GAS2) U95032 Q43903 CA513 hemoglobin alpha subunit V00491 P01922 CA518 trifunctional purine biosynthetic protein adenosine 3 X54199 P22102 major histocompatibility complex class II DM alpha CA528 subunit (HLA-DMA); RING6 X62744 P28067 CA532 cardiac ventricular myosin light chain 2 X66141 Q14908 CA533 adenylosuccinate synthetase; IMP-aspartate ligase X66503 P30520 CA540 uridine phosphorylase (UDRPase; UP) X90858 Q16831; Q15362 neutrophil gelatinase-associated lipocalin (NGAL); 25-kDa alpha-2-microglobulin-related subunit of CA546 MMP9; lipocalin 2; oncogene 24P3 X99133 P80188 CA547 adenine phosphoribosyltransferase (APRT) Y00486 P07741 CCAATenhancer-binding protein delta (C/EBP CU012 delta); nuclear factor-IL-6 beta protein (NF-IL6-beta)

DETL:

M83667 P49716; Q14937 CU038 DNA (cytosine-5-)-methyltransferase 2 (DNMT2) AJ223333 Q14717 CU041 retinoblastoma-related protein p107 L14812 P28749 ATP-binding cassette subfamily B (MDR1TAP) member 1 (ABCB1); multiple drug resistance 1 P08183; Q12755; CU043 protein (MOR1); P glycoprotein 1 (PGY1) M14758 Q14812 CU047 glutathione S-transferase mu 4 (GSTM4) M96233 Q03013 P11137; Q99976; CU048 microtubule-associated protein 2 (MAP2) U01828 Q99975 lysophosphatidic acid G protein-coupled endothelial Q92633; Q00722; CU120 differentiation receptor 2 (EDG2); vzg-1z U80811 Q00656; P78351 TTAGGG repeat binding factor 2 (hTRF2); E011 telomeric DNA-binding protein AF002999 Q15554 DNA polymerase epsilon subunit B; DNA E017 polymerase II subunit B AF025840 P56282 chondroitin sulfate proteoglycan 5 (CSPG5); E046 neuroglycan C (NOC) AF059274 Q95196 serine/threonine-protein kinase PAK-beta; p21 - E054 activated kinase 3 AF068864 Q75914 growth arrest & DNA damage-inducible protein 45 E065 gamma (GADD45 gamma) AF078078 none E069 cyclin D-binding MYB-like protein (hDMP1) AF084530 Q9Y222 E075 ribosomal protein kinase B (RSKB) AJ010119 Q75676 ferrochelatase; protoheme ferro-lyase; heme E077 synthetase D00726 P22830 proteasome (prosome, macropain) subunit alpha E081 type 3 (PSMA3); HC8 D00762 P25788 peripheral myelin protein 22 (PMP22); CD25 E083 protein; SR13 myelin protein D11428 Q01453 E096 photolyase/blue-light

receptor homolog D84657 Q16526 protein kinase C substrate 80-kDa protein heavy E102 chain (PKCSH); 80K-H protein J03075 P14314 E103 liver glucose transporter 2 J03810 P11168 serotransferrin (TF); siderophilin; beta-1-metal-E118 binding globulin M12530 P02787 DNA-binding protein A (DBPA); cold shock domain E123 protein A (CSDA) M24069 P16989; Q14121 26S protease regulatory subunit 6A; TAT-binding E126 protein 1 (TBP1); proteasome subunit p50 M34079 P17980 solute carrier family 9 member 1 (SLC9A1); sodium/hydrogen exchanger 1 (Na⁺ /H⁺ exchanger E130 1;NHE1) M81768 P19634 E132 B94 protein M92357 Q03169 RalGDSB; GTP/GDP dissociation stimulator for a E148 ras-related GTPase (RALGEF) U14417 Q12967 E153 selenium-binding protein U29091 Q13228 methionine aminopeptidase 2 (METAP2); peptidase M2; initiation factor 2-associated 67-kDa E154 glycoprotein U29607 P50579 E159 leptin receptor (LEPR); OB receptor (OBR); FA U43168 P48357 E160 myotubularin U46024 Q13496 sodium/potassium-transporting ATPase beta 3 subunit (ATPB3); sodium/potassium-dependent E161 ATPase U51478 P54709 alpha-1-acid glycoprotein 1 (AGP1); orosomucoid 1 E178 (OMD1) X02544 P02763 inter-alpha-trypsin inhibitor heavy chain H2 (ITI heavy chain H2); inter-alpha-trypsin inhibitor E181 complex component II X07173 P19823 carboxypeptidase H (CPH); CPE; enkephalin convertase; prohormone processing E185 carboxypeptidase X51405 P16870 E186 lactotransferrin; lactoferrin X53961 P02788 major epididymis-specific protein E4 (hE4); E188 epididymal secretory protein E4 X63187 Q14508 inter-alpha-trypsin inhibitor heavy chain H3 (ITI E190 heavy chain H3) X67055 Q06033 E193 tuberlin; tuberous sclerosis 2 protein (TSC2) X75621 P49815 E196 translin; recombination hotspot binding protein X78627 Q15631 dipeptidyl-peptidase 1 (DPP-1); cathepsin C; E198 cathepsin J; dipeptidyl transferase X87212 P53634 ATP-binding cassette 8 (ABC8); Drosophila white E199 homolog X91249 P45844 phosphatidylinositol-specific phospholipase C beta E210 3 (PLC-beta 3; PLCB3) Z16411 Q01970 E215 bystin L36720 Q13895 E219 acrosin-trypsin inhibitor II; HUSI II M91438 P20155 E220 emsl oncogene; cortactin (GUN); amplexin M98343 Q14247 autosomal dominant polycystic kidney disease II E228 (PKD2) U50928 Q13563 E230 organic cation transporter 1 U77086 Q15395 E231 alpha-fetoprotein; alpha-fetoglobulin V01514 P02771 E232 C-reactive protein X56692 P02741 E241 C-ets-2 J04102 P15036 heparin cofactor II (HCII); protease inhibitor E244 leuserpin 2 (hLS2) M12849 P05546 ALPHA-I-MICROGLOBULIN/INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) P02759; P00977; E252 (PROTEIN HG) (HI-30) (BIKUNIN) X04494 P02760 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN HI (ITI HEAVY CHAIN H1) (INTER-ALPHA- TRYPSIN INHIBITOR COMPLEX COMPONENT P78455; Q01746; E254 III) X63652 P19827 G014 PTH/PTHrP receptor L04308 Q03431 prostaglandin E2 receptor EP1 subtype (PTGER1); G021 prostanoid EPI receptor L22647 P34995 guanine nucleotide-binding protein G(K) alpha 3 G027 subunit (GNA3) M27543; J03198 P08754 guanine nucleotide-binding protein G(Y) alpha 11 P29992; Q14350; G037 subunit (GNA1 1) M69013 O15109 H001 delta 7-dehydrocholesterol reductase (DHCR7) AF034544 Q60492 squalene monooxygenase (SQLE); squalene H004 epoxidase (SE); ERG1 D78130 Q14534 H008 hydroxymethylglutaryl-CoA lyase L07033 P35914 CAAX-box farnesyltransferase alpha (FTase-alpha; H010 ENTA) L10413 P49354 H022 corticosteroid 11-beta-dehydrogenase isozyme 2 U14631 Q13194; P80365 H025 apolipoprotein AI (APOA1) X00566 P02647 H026 apolipoprotein CII (APQC2) X00568 P02655 H030 apolipoprotein B100 (APOBiQO) X04506 P04114 H039 mitochondrial hydroxymethylglutaryl-CoA synthase X83618 P54868 H040 rab geranylgeranyl transferase beta subunit Y08201 P53611; Q92697 H055 tissue inhibitor of metalloproteinase 3 (TIMP3) U14394 P35625

3-beta-hydroxy-delta-5-steroid dehydrogenase/steroid delta isomerase 1
 P14060; Q14545; H058 (HSD3B1); HSD3B2 M27137; M67466 P26439 H073 matrix
 metalloproteinase 2 (MMP2) J03210 P08253 sterol O-acyltransferase 1 (SOAT1);
 acyl-CoA: H078 cholesterol acyltransferase (ACAT) L21934 P35610 sterol
 regulatory element-binding transcription H081 factor 1 U00968 P36956 H085
 oxysterol-binding protein (OSBP) M8691 7; J04757 P22059 H092 apolipoprotein
 CIV (APOG4) U32576 P55056 H094 mitochondrial glycerol-3-phosphate
 dehydrogenase U12424 P43304 H099 alcohol sulfotransferase L20000 Q06520 H103
 angiotensinogen (AGT) K02215 P01019 H104 renin L00073 P00797 H105
 angiotensin 1 converting enzyme J04144 P12821 H108 endothelin 1 (ET1) Y00749
 P05305 H115 alcohol dehydrogenase 5 clii polypeptide M30471 P11766 H116
 alcohol dehydrogenase class II pi subunit M15943 P08319 alpha 1 B adrenergic
 receptor (ADRA1 B); alpha 1 B H134 adrenoreceptor U03865 P35368 hydroxysteroid
 17-beta dehydrogenase 3 (HSD17B3); estradiol 17-beta dehydrogenase 3 H149
 (EDH17B3) U05659 P37058 brain fatty acid-binding protein (B-FABP); FABP7;
 H152 brain lipid-binding protein (BLBP) AJ002962 O15540; O14951 H156
 caveolin2 AF035752; U32114 P51636 caveolin 3 (CAV3); limb-girdle muscular
 dystrophy H157 type IC (LGMD1C); VIP21 AF043101 P56539 H159 LDL-associated
 phospholipase A2 U20157 Q15692; Q13093 vasoactive intestinal polypeptide
 receptor 2 P41587; Q15870; H166 (VIPR2); pituitary adenylated cyclase
 activating L40764 Q13053 polypeptide receptor 3 (PACAP3 receptor; PACAPR3);
 helodermin-preferring receptor nuclear receptor subfamily 3 group C member 1
 (NR3C1); lymphocyte glucocorticoid receptor (GRL; H170 GCR) M10901 P04150;
 P04151 H178 steroid receptor coactivator 1 (SRC1) U59302 Q00150
 estrogen-related receptor alpha (ERR-alpha; H180 ESRRA); estrogen
 receptor-like 1 (ESRL1) X51416; Y00290 P11474; O14514 H194 prothrombin;
 coagulation factor II V00595 P00734 Q16001; Q15190; H196 autoproteolysis IIA
 X02750 Q15189; P04070 H201 amyloid-like protein 2 S60099 Q06481 H207 signal
 transducer CD24 M58664 P25063 H209 macrolsialin S57235 P34810 H210 selectin
 P ligand U02297 Q14242; Q12775 H218 alpha-2-antiplasmin D00174 P08697 H222
 GAP junction alpha-4 protein M96789 P35212 H238 protein 4.1 M14993 P11171
 H241 vinculin M33308 P18206 ubiquitously expressed nuclear receptor (U N R;
 NER); nuclear receptor subfamily 1 group H member 2 (NR1 H2); oxysterols
 receptor LXR beta

PGPUB-DOCUMENT-NUMBER: 20010051335
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20010051335 A1

TITLE: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

PUBLICATION-DATE: December 13, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
LALGUDI, RAGHUNATH V.	CLAYTON	MO	US	
ITO, LAURA Y.	PLEASANTON	CA	US	
SHERMAN, BRADLEY K.	OAKLAND	CA	US	

US-CL-CURRENT: 435/6,435/69.1

ABSTRACT:

The present invention provides purified, corn tassel-derived polynucleotides (cdps) which encode corn tassel-derived polypeptides (CDPs). The invention also provides for the use of cdps or their complements, oligonucleotides, or fragments in methods for determining altered gene expression, to recover regulatory elements, and to follow inheritance of desirable characteristics through hybrid breeding programs. The invention further provides for vectors and host cells containing cdps for the expression of CDPs. The invention additionally provides for (i) use of isolated and purified CDPs to induce antibodies and to screen libraries of compounds and (ii) use of anti-CDP antibodies in diagnostic assays.

DATE FILED: April 16, 1999

----- KWIC -----

DETL:

Zea mays SU1 isomylase (sugaryl) gene, complete cds. 700345362H1 g557681 52
-32 gb105pln Z. mays mRNA for ribosomal protein S28. 700344996H1 g2829865 46
-23 gb105eukp F3I6.4 700343840H1 g2511530 79 -67 gb105pln Eleusine indica
alpha tubulin 1 (TUA1) mRNA, complete cds. 700342780H1 g620050 16 -11
gb105eukp T15H9.1 700345826H1 g902524 72 -75 gb105pln Zea mays clone MubG10
ubiquitin fusion protein gene, complete cds. 700345562H1 g493588 61 -54
gb105pln Hordeum vulgare disulfide isomerase (PDI) mRNA, complete cds.
700379651H1 g474003 27 6 gb105pln Rice mRNA, partial homologous to ribosomal
protein rp21c gene. 700344871H1 g1526426 9 7 gb105allp proteasome subunit p42
700344496H1 g458426 9 7 gb105eukp dihydrolipoamide acetyltransferase
700281806H2 g624220 64 -23 gb105pln Oryza sativa signal recognition particle
19 kDa protein subunit SRP19 mRNA, complete cds. 700346719H1 g2668739 95 -90
gb105pln Zea mays translation initiation factor GOS2 (TIF) mRNA, complete cds.

700345120H1 g2668749 45 -33 gb105pln Zea mays ribosomal protein L30 (rpl30) mRNA, complete cds. 700343484H1 g836943 19 -11 gb105pln Arabidopsis thaliana calcium-dependent kinase (CDPK6) gene, complete cds. 700380557H1 g416252 29 -16 gb105pln Rice mRNA for 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, partial sequence. 700344155H1 g498906 31 -29 gb105eukp RPL27-5; ribosomal protein L27 homolog 700346835H1 g1100222 35 -23 gb105pln Pinus sylvestris chloroplast NAD⁺-dependent glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds. 700346790H1 g509264 23 -13 gb105pln B. napus mRNA for acyl-CoA binding protein. 700343740H1 g425274 7 5 gb105eukp synaptotagmin, p65 700343065H1 g248338 39 -42 gb105pln polyubiquitin [maize, Genomic, 3439 nt]. 700343038H1 g904027 44 -33 gb105pln Triticum aestivum nucleosome assembly protein I mRNA, partial cds. 700345539H1 g22118 13 16 gb105pln Z. mays DNA for Adh1-Cm allele. 700344895H1 g387112 35 -26 gb105allp 34 kDa beta-galactoside-binding lectin (L-34) 700281810H2 g2529253 25 -0 gb105eukp rpb12; RNA polymerase II subunit Rpb12; EC 2.7.7.6 700342830H1 g2668737 52 -49 gb105pln Zea mays translation initiation factor 5A (TIF5A) mRNA, complete cds. 700380650H1 g168500 57 -45 gb105pln Maize (Zea mays) histone H4 gene (H4C14), complete cds. 700346888H1 g899607 68 -36 gb105pln Zea mays polyubiquitin (MubC5) mRNA, complete cds. 700343322H1 g1657763 13 10 gb105pln Zea mays retrotransposon Ji-3 5' LTR and primer binding site DNA sequence. 700343295H1 g2760839 15 -2 gb105eukp F18A8.10; putative receptor kinase 700380070H1 g1435156 50 -6 gb105pln L. esculentum mRNA for histone H3 variant H3.3. 700343623H1 g1322844 22 -6 gb105eukp SPT16 700342343H1 g602398 20 -2 gb105eukp SPF1; P-type ATPase 700343717H1 g600390 17 -1 gb105pln A. thaliana UbcAT4b mRNA for ubiquitin conjugating enzyme E2. 700281969H2 g2791884 18 -3 gb105pln Arabidopsis thaliana JAB1 (JAB1) mRNA, complete cds. 700281967H1 g514945 54 -82 gb105pln Zea mays sucrose synthase (Sus1) mRNA, complete cds. 700347133H1 g1668706 51 0 gb105eukp atran2 700346930H1 g2827559 8 8 gb105eukp T12H17.210; predicted protein 700343874H1 g2827650 27 -13 gb105eukp F18F4.60; potassium transporter-like protein 700344108H1 g1206016 14 12 gb105pln Yeast (Schizosaccharomyces pombe) ribosomal protein L5 gene, complete cds. 700346968H1 g1864002 23 -35 gb105pln Nicotiana tabacum mRNA for 21D7, complete cds. 700346207H1 g141900 8 6 gb105allp alcohol dehydrogenase (EC 1.1.1.1) 700281877H2 g456508 47 -27 gb105pln A. thaliana ASK-gamma mRNA. 700380172H1 g2414643 28 -15 gb105pln Yeast (Saccharomyces pombe) chromosome I cosmid c3H5. 700346992H1 g2443472 41 -19 gb105eukp SF2; ASF/SF2 homolog 700346309H1 g312178 32 -52 gb105pln Z. mays GapC2 gene. 700345729H1 g1272634 13 1 gb105eukp K07C5.4 700344480H1 g2564051 39 -1 gb105pln Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence. 700345085H1 g1755008 76 -66 gb105pln Triticum aestivum calmodulin TaCaM4-1 mRNA, complete cds. 700343811H1 g2459531 27 -14 gb105eukp Mf-FatB1; acyl-ACP thioesterase 700342716H1 g2288886 24 -9 gb105pln Arabidopsis thaliana mRNA for mevaolonate diphosphate decarboxylase. 700345974H1 g2827001 63 -12 gb105pln Triticum aestivum 70 kDa heat shock protein (TaHSP70d) mRNA, complete cds. 700343574H1 g2267005 35 -19 gb105pln Oryza sativa endosperm lumenal binding protein (BiP) mRNA, complete cds. 700343059H1 g577611 70 -83 gb105pln Zea mays CRT1 gene for calcium-binding protein. 700342287H1 g459017 6 -4 gb105eukp atp6; subunit 6 of the ATPase complex 700342532H1 g1438971 6 5 gb105allp potassium channel Kv8.1 700347070H1 g2246455 19 -1 gb105pln Arabidopsis thaliana S-adenosyl-methionine-sterol-C-methyltransferase mRNA, complete cds. 700343890H1 g1845194 41 -59 gb105pln Z. mays mRNA for HMGc1 protein. 700343209H1 g1770036 15 1 gb105allp hypothetical protein 700380711H1 g2827081 39 -37 gb105pln Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA,

complete cds. 700379992H1 g556409 12 4 gb105eukp RITA-1; transcriptional activator protein 700344220H1 g391602 34 -34 gb105pln *Arabidopsis thaliana* mRNA for casein kinase II catalytic subunit. 700346872H1 g1245870 15 3 gb105allp replication factors MCM = dpa [*Drosophila*, Peptide, 866 aa] 700346067H1 g349405 14 17 gb105pln *Brassica napus* (clone BnNa) DNA sequence. 700344372H1 g285999 18 3 gb105allp KIAA0017 700346883H1 g2262163 34 -7 gb105eukp F5J6.8; hypothetical protein similar to F5J6.10 700344784H1 g1248203 14 7 gb105allp Synthetic mature subtilisin 309 gene 700344201H1 g415316 22 -23 gb105pln Rice mRNA for acidic ribosomal protein P0, complete cds. 700344836H1 g2689242 27 -5 gb105pln *A. thaliana* mRNA for ubiquitin conjugating enzyme UBC2. 700347390H1 g2160160 44 -25 gb105eukp F21M12.5 700342828H1 g2414643 23 -4 gb105pln Yeast (*Saccharomyces pombe*) chromosome I cosmid c3H5. 700380444H1 g643596 33 -9 gb105pln Corn mRNA for cysteine proteinase, clone CCP, complete cds. 700343339H1 g2736191 15 5 gb105allp DfrA 700342484H1 g1360177 12 7 gb105allp ORF YLL011w 700380569H1 g8040 25 -0 gb105eukp histone H2A variant (AA 1-141) 700343166H1 g2351577 19 -2 gb105pln *Prunus armeniaca* adenylate kinase homolog mRNA, complete cds. 700344091H1 g1132482 38 -18 gb105pln Rice mRNA for ADP-ribosylation factor, complete cds. 700343229H1 g168543 100 -36 gb105pln Zea mays putative ribosomal protein S8 mRNA, partial cds. 700343924H1 g459199 18 7 gb105pln *Gossypium hirsutum* vacuolar H⁺-ATPase subunit B mRNA, partial cds. 700343660H1 g1009237 52 -53 gb105pln *Tupeia antarctica* (Forst. f.) Chamb. and Schlecht. 18S ribosomal RNA gene, partial sequence. 700342370H1 g21796 58 -47 gb105pln Wheat histone H3 gene. 700347302H1 g2599103 7 15 gb105pln *Dunaliella salina* 60S ribosomal protein (DSRP1) mRNA, complete cds. 700343219H1 g1401233 17 3 gb105pln *Pinus taeda* water deficit inducible protein LP3-3 (lp3-3) mRNA, partial cds. 700346088H1 g1360388 6 7 gb105eukp ORF YLR051c 700343157H1 g644492 80 -79 gb105pln Corn elongation factor 1alpha gene, complete cds. 700342896H1 g1469220 35 -8 gb105pln *B. oleracea* mRNA (unknown). 700342446H1 g1051257 59 -48 gb105pln *Hordeum vulgare* vacuolar ATPase catalytic subunit mRNA, partial cds. 700345652H1 g203604 59 2 gb105allp contiguous repeat polypeptide 700344609H1 g1732515 9 5 gb105allp myosin heavy chain-like protein 700344191H1 g2408032 11 6 gb105allp hypothetical protein 700342352H1 g2353331 25 -14 gb105eukp rpS19; ribosomal protein S19 700344194H1 g508307 30 -17 gb105pln *Arabidopsis thaliana* protein-serine kinase mRNA, complete cds. 700344010H1 g473604 9 14 gb105pln Zea mays W-22 histone H2B mRNA, complete cds. 700347001H1 g1906827 54 -44 gb105pln *A. thaliana* hsp81.4 gene. 700344191H1 g1688076 10 7 gb105allp tetratricopeptide repeat protein 700342482H1 g169589 13 4 gb105eukp U2B; U2snRNP-specific protein; spliceosomal protein 700347067H1 g1772495 6 6 gb105eukp HMB-CoA synthase; hydroxymethylglutaryl-CoA synthase; EC 4.1.3.5 700345565H1 g1724101 58 -46 gb105pln *Mesembryanthemum crystallinum* S-adenosyl-L-homocystein hydrolase mRNA, complete cds. 700343332H1 g603601 15 -0 gb105eukp NTF2; Ntf2p: Nuclear Transport Factor 2 700379666H1 g168500 25 -44 gb105pln Maize (*Zea mays*) histone H4 gene (H4C14), complete cds. 700347314H1 g533251 26 -19 gb105pln Zea mays (clone pSM8) sucrose synthase 2 (Sus1) gene, complete cds. 700343045H1 g2190976 12 4 gb105allp macrophage migration inhibitory factor 700343386H1 g486551 11 7 gb105allp ORF YKR076w 700281876H2 g2414402 28 -17 gb105eukp Y57G11C.15 700380593H1 g168639 41 -74 gb105pln Zea mays autonomous transposable element En-1 mosaic protein gene, complete cds. 700343157H1 g2282583 83 -81 gb105pln Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds. 700344005H1 g736271 51 -25 gb105pln *O. sativa* hsp70 gene for heat shock protein 70. 700347378H1 g2668748 31 -19 gb105eukp rp117;

ribosomal protein L17 700346242H1 g450548 36 -16 gb105pln *O. sativa* (pRSAM-1) gene for S-adenosyl methionine synthetase. 700379824H1 g403228 19 7 gb105allp ribonucleotide reductase small subunit 700346865H1 g474009 65 -49 gb105pln Rice mRNA, partial homolog to ribosomal protein S19 gene. 700343526H1 g2244881 15 3 gb105eukp PDR5-like ABC transporter 700344660H1 g452712 40 -6 gb105eukp beta-galactosidase; EC 3.2.1.23 700342367H1 g902585 44 -64 gb105pln Zea mays clone MubG9 ubiquitin gene, complete cds. 700379726H1 g496271 23 -2 gb105pln *Nicotiana tabacum* small Ras-like GTP-binding protein (Ran-B1) mRNA, complete cds. 700343063H1 g2245029 11 6 gb105eukp limonene cyclase homolog 700346629H1 g218182 40 -22 gb105pln Rice mRNA for oryzain beta (EC 3.4.22). 700344132H1 g1786871 8 7 gb105allp f311; 100 pct identical to fragment YBEK_ECOLI SW: P41409 (123 aa) but contains 188 additional C-ter residues 700344316H1 g1420686 14 -2 gb105eukp RPL18B 700345189H1 g602301 13 14 gb105pln *Arabidopsis thaliana* diminuto (DIM) mRNA, complete cds. 700344065H1 g291927 46 -4 gb105allp cystatin B 700344170H1 g16086 23 -4 gb105pln *A. porrum* dnaJ mRNA for DNA J protein (partial). 700343466H1 g17645 49 -5 gb105allp RIBOSOMAL PROTEIN L35a 700342763H1 g2689469 19 3 gb105eukp IAA22 700346208H1 g218334 34 -32 gb105pln *Triticum aestivum* mRNA for O-acetylserine (thiol) lyase. 700343436H1 g1872521 20 -5 gb1053eukp LSD1; negative regulator of cell death; zinc-finger protein Lsd1 700379728H1 g387908 36 -32 gb105pln *Brassica rapa* S-phase-specific (BIS289) mRNA, complete cds. 700346636H1 g22324 33 -23 gb105pln *Z. mays* mRNA for H2B histone (clone ch2B221).

PGPUB-DOCUMENT-NUMBER: 20010034023
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20010034023 A1

TITLE: Gene sequence variations with utility in determining the treatment of disease, in genes relating to drug processing

PUBLICATION-DATE: October 25, 2001 .

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Stanton, Vincent P. JR.	Belmont	MA	US	
Zillmann, Martin	Shrewsbury	MA	US	

US-CL-CURRENT: 435/6,702/20

ABSTRACT:

Methods for identifying and utilizing variances in genes relating to efficacy and safety of medical therapy and other aspects of medical therapy are described, including methods for selecting an effective treatment.

DATE FILED: December 7, 2000

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
WO	PCT/US00/01392	2000WO-PCT/US00/01392	January 20, 2000

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DETL:

PLA2G2A M22430 172411 GEN-25V Human RASF-A PLA2 mRNA, complete cds 231 96G>C Silent 267 132C>T Silent 278 143-144delGT Frame 643 508C>T 3' 700 565G>C 3' PNMT J03727 171190 GEN-120 Human phenylethanolamine N-methyltransferase mRNA, complete cds 462 456A>G Silent 568 562A>T S188C 638 632T>A L211H 656 650T>A L217Q 767 761G>A R254H 832 826T>A W276R PTAFR M76674 173393 GEN-3P9 Platelet-activating factor receptor 696 671C>A A224D S77127 S77127 None GEN-MTU Superoxide dismutase 2 (manganese), promoter and genomic 1183 1183C>T Genomic 1735 1735T>C Genomic 4903 4903G>A Genomic 7939 7939G>A Genomic SLC12A3 U44128 600968 GEN-CCX Human thiazide- sensitive Na-Cl cotransporter (hTSC) mRNA, complete cds 1884 1884G>A Silent 2142 2142C>T Silent 2625 2625C>T Silent SLC2A4 M20747 138190 GEN-23Q Human insulin- responsive glucose transporter (GLUT4) mRNA, complete cds 378 233C>G T78S 535 390C>T Silent SLC6A1 X54673 137165 GEN-358 H.sapiens GAT1 mRNA for GABA transporter 240 6G>A Silent 885 651G>T Silent SLC6A3 L24178 126455 GEN-283 Homo sapiens dopamine transporter mRNA, complete cds 133 114C>T Silent 169

150G>T Silent 181 162C>T Silent 729 710G>A R237Q 1234 1215G>A
 Silent 1750 1731C>T Silent SOD3 J02947 185490 GEN-Y3 Human extracellular-
 superoxide dismutase (SOD3) mRNA, complete cds 760 691C>G R231G TAP2
 Z22935 170261 GEN-26P H.sapiens TAP2B mRNA, complete CDS 1690 1662G>A
 Silent 1746 1718A>G D573G 2021 1993G>A A665T TCN2 M60396 275350
 GEN-3AX Human transcobalamin II (TCII) mRNA, complete cds 813 776C>G P259R
 1623 1586C>A 3' 1635 1598C>A 3' TGFB3 L07594 600742 GEN-1EA Human
 transforming growth factor-beta type III receptor (TGF-beta) mRNA, complete
 cds 150 (-199)G>A 5' 150 (-199)G>C 5' 3957 3609A>C 3' 3966
 3618G>C 3' TPMT U12387 187680 GEN-1LY Human thiopurine methyltransferase
 (TPMT) mRNA, complete cds 314 238G>C A80P 536 460G>A A154T 720
 644G>A R215H 795 719A>G Y240C TRP2 M55169 190470 GEN-35U Homo sapiens
 tripeptidyl peptidase II mRNA, 3' end 3637 3637G>A 3' U00672 U00672 146933
 GEN-4A Interleukin 10 receptor 3524 3463A>G 3' U04636 U04636 600262
 GEN-MVG Cyclooxygenase 2, genomic sequence (not including promoter) 671
 671C>G Genomic 841 841T>G Genomic 2191 2191C>G Genomic 4719
 4719T>C Genomic 5310 5310T>C Genomic 6551 6551A>G Genomic 6620
 6620T>C Genomic 6843 6843C>A Genomic 7330 7330T>C Genomic 7401
 7401G>A Genomic U06088 U06088 253000 GEN-MP3 Human N- acetylgalactosamine
 6-sulphatase (GALNS) gene 708 708T>C Silent U08092 U08092 None GEN-4C
 Histamine N-methyltransferase 353 314T>C I105T 978 939G>A 3' U09178
 U09178 274270 GEN-HA Dihydropyrimidine Dehydrogenase 143 62G>A R21Q 166
 85T>C C29R 784 703C>T R235W 1084 1003G>C V335L 1237 1156G>T
 Frame 1682 1601G>A S534N 1708 1627A>G I543V 2275 2194G>A V7321I
 2738 2657G>A R886H 3002 2921A>T D974V 3064 2983G>T V995F U09806
 U09806 236250 GEN-4FZ Human methylenetetrahydrofolate reductase mRNA, partial
 cds 120 120T>C Silent 473 473G>A R158Q 550 550C>T Frame 668
 668C>T A223V 1059 1059T>C Silent 1289 1289C>A 3' 1308 1308T>C
 3' U10417 U10417 601295 GEN-1IX Homo sapiens ileal sodium-dependent bile acid
 transporter (SLC10-A2) mRNA, complete cds 1109 511G>T A171S 1326 728T>C
 L243P 1383 785C>T T262M U14510 U14510 602698 GEN-1RD Human transcription
 factor NFATx mRNA, complete cds 3564 3540A>C 3' U14650 U14650 602243
 GEN-1RL Human platelet- endothelial tetraspan antigen 3 mRNA, complete cds
 1263 1204G>C 3' U16660 U16660 600696 GEN-1YD Human peroxisomal enoyl-CoA
 hydratase-like protein (HPXEL) mRNA, complete cds 149 122A>C E41A U19487
 U19487 176804 GEN-4I "PROSTAGLANDIN E2 RECEPTOR, EP2 SUBTYPE" 1442
 1286A>G 3' U36601 U36601 603268 GEN-IR Heparan N-
 deacetylase/N-sulfotransferase-2 2727 2700T>G 3' 2972 2945A>G 3'
 U37519 U37519 601917 GEN-2OF Human aldehyde dehydrogenase (ALDH8) mRNA,
 complete cds 1871 1255C>T 3' U49516 U49516 312861 GEN-1Q Serotonin 5-HT
 receptors 5-HT2C 796 68G>C C23S 2831 2103T>G 3' U50040 U50040 601582
 GEN-2ZR Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA,
 complete cds 2882 2866C>T H956Y U68162 U68162 159530 GEN-MJM Human
 thrombopoietin receptor (MPL) gene 218 152C>T A51V 547 481G>A E161K
 U73338 U73338 156570 GEN-69 Methionine Synthase 6750 6356G>A 3' U83411
 U83411 603105 GEN-3Y1 Homo sapiens carboxypeptidase Z precursor, mRNA,
 complete cds 1788 1749G>A Silent X02612 X02612 None GEN-MW2 Cytochrome
 P450 CYP1A1, promoter and genomic 6819 6819G>A Genomic 7569 7569T>C
 Genomic X02812 X02812 190180 GEN-XR Human mRNA for transforming growth
 factor-beta (TGF-beta) 870 29C>T P10L 915 74C>G P25R 1632 791C>T
 T264I X02920 X02920 107400 GEN-PH Human mRNA for alpha 1-antitrypsin
 carboxyterminal region (aa 268-394) 195 195C>T Silent 327 327A>C E109D
 X03348 X03348 138040 GEN-PL Human mRNA for beta-glucocorticoid receptor (clone

OB10) 198 66G>A Silent 200 68G>A R23K 325 193T>G F65V 936
804C>T Silent 1220 1088A>G N363S 1226 1094A>G N365S 3134
3002G>T 3' 3669 3537A>G 3' X03438 X03438 138970 GEN-PM Human mRNA for
granulocyte colony-stimulating factor (G-CSF) 1180 1149C>T 3' X03663
X03663 164770 GEN-51 Colony stimulating factor 1 receptor 3206 2906A>G
Y969C 3807 3507G>C 3' X03747 X03747 182330 GEN-KR ATPase, Na⁺/K⁺
transporting, beta 1 polypeptide 1773 1647C>T 3' X08006 X08006 124030
GEN-1FE Human mRNA for cytochrome P450 db1 100 100C>T P34S 124 124G>A
G42R 137 137 138insT Frame 271 271C>A L91M 281 281A>G H94R

US-PAT-NO: 6383784

DOCUMENT-IDENTIFIER: US 6383784 B1

TITLE: Construction of nucleoprotein based assemblies comprising addressable components for nanoscale assembly and nanoprocessors

DATE-ISSUED: May 7, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Smith; Steven S.	Los Angeles	CA	N/A	N/A

US-CL-CURRENT: 435/91.2,435/6 ,536/22.1

ABSTRACT:

A nucleoprotein based nanoprocessor is described. The nanoprocessor includes one or more chimelic fusion proteins linked to a DNA scaffold. Both components of the fusion protein are enzymes.

11 Claims, 14 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 8

DATE FILED: December 3, 1999

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DEPR:

Catabolite-gene Activator Protein (CAP) is a positive transcription factor from E. coli which activates transcription from promoters sensitive to catabolite repression. It acts as a dimer in the presence of cyclic AMP (cAMP) by binding to its DNA recognition sequence and inducing it to bend. The crystal structure of the bent-DNA has been obtained (22) and visual inspection of the 3-D model of the structure available from the Brookhaven protein database suggests that pro9 at the N-terminus could be used in a head to tail linkage placing a bacterial methyltransferase in front of the CAP protein without disrupting the capacity of the protein to interact with itself in the dimer or with its DNA recognition site.

US-PAT-NO: 6362007

DOCUMENT-IDENTIFIER: US 6362007 B1

TITLE: Methylated, SMD homologous peptides, reactive with the antibodies from sera of living beings affected with systemic lupus erythematosus

DATE-ISSUED: March 26, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Meheus; Lydie	Merelbeke	N/A	N/A	BEX
Union; Ann	Aalter	N/A	N/A	BEX
Raymackers; Joseph	Eke	N/A	N/A	BEX
Luhrmann; Reinhard Georg	Marburg	N/A	N/A	DEX

US-CL-CURRENT: 436/506,436/518 ,530/324

ABSTRACT:

The present invention relates to a method of producing certain peptides containing methylated arginines that are followed by a glycine residue and that constitute immunogenic determinants of antibodies present in sera from patients with systemic lupus erythematosus, or Epstein-Barr virus and wherein the methylation is a prerequisite for reacting with said antibodies. The invention also relates to the use of said peptides for diagnosis and treatment of systemic lupus erythematosus and related diseases, and diseases in which Epstein-Barr virus has been implicated.

9 Claims, 5 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 3

DATE FILED: May 10, 1999

----- KWIC -----

BSPR:

According to a more specific embodiment the present invention also relates to a method for producing any of the above mentioned peptides, by classical chemical synthesis, wherein methylated arginines are substituted for unmethylated arginine residues at certain steps during the chemical synthesis. The present invention also relates to a method for producing any of the above mentioned peptides, wherein the primary amino acid sequence is produced by classical chemical synthesis, and wherein the arginine residues that precede glycine residues are subsequently methylated by contacting said peptides with a protein arginine methyltransferase. The present invention also relates to a method for producing any of the above mentioned peptides comprising the following steps: (i) transforming an appropriate cellular host with a recombinant vector in which a polynucleic acid is inserted comprising the sequence that codes for said peptide under the control of the appropriate regulatory elements such that said peptide or a protein comprising said peptide is expressed and/or secreted, (ii) culturing said transformed cellular host under conditions allowing expression of said protein or peptide and allowing a partial or optimal methylation of the arginines present in said peptide, and (iii) harvesting said

peptide. The present invention also relates to a method for producing any of the above mentioned peptides comprising the following steps: (i) transforming an appropriate cellular host with a recombinant vector in which a polynucleic acid is inserted comprising the sequence that codes for said peptide under the control of the appropriate regulatory elements, such that said peptide or a protein comprising said peptide is expressed and/or secreted, (ii) culturing said transformed cellular host under conditions allowing expression of said protein or said peptide, (iii) harvesting said protein or said peptide, and (iv) methylating arginine residues of said protein or said peptide by contacting with a protein arginine methyltransferase. According to a more specific embodiment the present invention also relates to any of the above mentioned methods, wherein said host cell is a bacterial host or yeast or any other eukaryotic host cell which is preferably transformed with a recombinant baculovirus.

US-PAT-NO: 6355450

DOCUMENT-IDENTIFIER: US 6355450 B1

TITLE: Computer readable genomic sequence of Haemophilus influenzae Rd, fragments thereof, and uses thereof

DATE-ISSUED: March 12, 2002

INVENTOR-INFORMATION:

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US-CL-CURRENT: 435/69.1,435/252.3 ,435/320.1 ,435/851 ,536/23.1 ,536/23.7 ,536/24.32 ,536/24.33

ABSTRACT:

The present invention provides the sequencing of the entire genome of Haemophilus influenzae Rd, SEQ ID NO: 1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies over 1700 protein encoding fragments of the genome and identifies, by position relative to a unique Not I restriction endonuclease site, any regulatory elements which modulate the expression of the protein encoding fragments of the Haemophilus genome.

88 Claims, 47 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 47

DATE FILED: June 7, 1995

----- KWIC -----

DETL:

HI0200 214274 215227 msbB protein (msbB) (Escherichia coli) 45.3 67.0 301
HI0411 429238 430662 msbB protein (msbB) (Escherichia coli) 50.9 69.3 284
HI0712 756824 757117 negative regulator of translation (retB) (Escherichia coli) 28.3 48.3 60 HI0631 667822 668406 negative rpo regulator(mclA) (Escherichia coli) 40.1 62.9 199 HI0269 299532 301232 nitrate sensor protein (narO) (Escherichia coli) 38.6 63.0 555 HI0728 778003 777380 nitrate/nitrite response regulator protein (narP) (Escherichia coli) 59.6 79.3 205 HI0339 363915 364250 nitrogen regulatory protein P-H (glnB) (Escherichia coli) 77.7 93.8 112 HI1747 1828067 1826037 penta-phosphate guanosine-J pyrophosphohydrolase (spoT) (Escherichia coli) 58.8 76.8 675 HI0200 214274 215227 phosphate regulon sensor protein (phoR) (Escherichia coli) 41.8 66.8 335 HI1382 1475709 1475017 phosphate regulon transcriptional regulatory protein (phoB) (Escherichia coli) 52.9 71.8 227 HI0765 827030 825768 probably nadAB transcriptional regulator (nedR) (Escherichia coli) 54.6 75.1 349 HI1641 1697003 1698115 punne necleotide synthesis repressor protein (purR)

(Escherichia coli) 55.9 74.5 326 HI0164 178405 178713 putative murein gene
 regulator (bolA) (Escherichia coli) 47.1 65.7 102 HI0508 522278 523273 rbs
 repressor (rbsR) (Escherichia coli) 48.8 71.0 329 HI0565 582225 581776
 regulatory protein (asnC) (Escherichia coli) 68.0 81.0 147 HI1617 1677452
 1676583 regulatory protein sfs1 involved in maltose metabolism (srsA)
 (Escherichia coli) 54.3 71.2 218 HI0995 946128 946688 repressor for
 cytochrome P450 (Bm3R1) (Bacillus magatenum) 23.3 50.5 182 HI0271 302396
 303238 RNA polymerase sigma-32 factor (heat shock regulatory protein F334)
 70.8 86.8 281 (rpoH) (Escherichia coli) HI0535 555646 557532 RNA polymerase
 sigma-70 factor (rpoD) (Escherichia coli) 68.9 80.8 608 HI0630 667228 667794
 RNA polymerase sigma-E factor (rpoE) (Escherichia coli) 73.0 87.8 189 HI1713
 1781137 1779785 sensor protein for basR (basS) (Escherichia coli) 30.0 55.7
 253 HI1444 1529117 1528668 stringent starvation protein (sspB) (Escherichia
 coli) 63.2 81.1 106 HI1445 1529755 1529120 stringent starvation protein A
 (sspA) (Haemophilus somnus) 76.9 87.3 212 HI1745 1815630 1814704
 trans-activator of metE and metH (metR) (Escherichia coli) 39.5 60.8 294
 HI0360 382477 383121 transcription activator (tenA) (Bacillus subtilis) 27.8
 48.3 208 HI0883 722643 721766 transcriptional activator protein (xlvY)
 (Escherichia coli) 47.4 70.3 293 HI1714 1781799 1781137 transcriptional
 regulatory protein (basR) (Escherichia coli) 43.5 59.7 216 HI0412 430780
 431783 transcriptional regulatory protein (tyrR) (Escherichia coli) 48.2 65.8
 306 HI0832 880611 880913 tryptophan repressor (trpR) (Emerobacter aerogenea)
 38.8 67.0 88 HI0054 54188 54965 uxu operon regulator (uxuR) (Escherichia coli)
 50.0 72.1 246 HI1109 1170415 1169255 xylose operon regulatory protein (xylR)
 (Escherichia coli) 57.3 75.3 384 Replication DNA - replication,
 repair/modification, recombination HI0751 822003 823136 A/G-specific adenine
 glycosylase (muyY) (Escherichia coli) 81.9 75.1 341 HI0895 1056874 1055313
 chromosomal replication initiator protein (dnaA) (Escherichia coli) 61.7 79.7
 464 HI1229 1294415 1294317 chromosomal replication initiator protein (dnaA)
 (Escherichia coli) 50.0 75.0 12 HI0316 345720 345151 crossover junction
 endonuclease (ruvC) (Escherichia coli) 78.5 88.3 163 HI0955 1011537
 1012736 dtp protein (dtp) (Escherichia coli) 61.1 76.8 402 HI0210 223259
 224116 DNA adenine methylase (dam) (Escherichia coli) 55.4 71.4 268 HI1267
 1343755 1341116 DNA gyrase, subunit A (gyrA) (Escherichia coli) 70.6 84.8 859
 HI0569 587397 584980 DNA gyrase, subunit B (gyrB) (Escherichia coli) 74.7 85.9
 803 HI1191 1255302 1253122 DNA helicase II (uvrD) (Haemophilus influenzae)
 96.8 97.5 727 HI1102 1162989 1160953 DNA ligase (lig) (Escherichia coli) 63.7
 79.9 666 HI0405 423539 424207 DNA mismatch protein (mutH) (Escherichia coli)
 60.4 80.7 212 HI0709 750565 753147 DNA mismatch repair protein (mutS)
 (Escherichia coli) 71.0 84.0 853 HI0067 69622 71508 DNA mismatch repair
 protein MUTL (mutL) (Escherichia coli) 50.2 67.3 612 HI0858 904919 902130 DNA
 polymerase I (polA) (Escherichia coli) 63.1 77.0 928 HI0994 1055297 1054200
 DNA polymerase III beta-subunit (dnaN) (Escherichia coli) 62.6 80.3 366
 HI0457 476761 475763 DNA polymerase III delta prime subunit (holB)
 (Escherichia coli) 35.3 57.4 316 HI0925 979730 980761 DNA polymerase III delta
 subunit (holA) (Escherichia coli) 45.2 62.0 332 HI0138 152669 151902 DNA
 polymerase III epsilon subunit (dnaO) (Escherichia coli) 61.3 76.5 236 HI0741
 799019 795544 DNA polymerase III, alpha chain (dnaE) (Escherichia coli) 71.9
 85.7 1159 HI1402 1493690 1493259 DNA polymerase III, chi subunit (holC)
 (Haemophilus influenzae) 95.9 98.9 88 HI0011 11672 11271 DNA polymerase III,
 psi subunit (holD) (Escherichia coli) 34.4 59.2 123 HI0534 553659 555645 DNA
 primase (dnaG) (Escherichia coli) 56.5 73.8 571 HI1746 1826037 1823959 DNA
 recombinase (recG) (Escherichia coli) 68.5 80.1 893 HI0070 77166 75493 DNA

repair protein (recN) (*Escherichia coli*) 48.6 67.3 833 HI0659 699507 700058
 DNA topoisomerase I (topA) (*Bacillus subtilis*) 34.2 55.0 110 HI0656 698124
 697570 DNA-3-methyladenine glycosidase I (lagI) (*Escherichia coli*) 62.6 76.0
 179 HI0730 779457 781969 DNA-dependent ATPase, DNA helicase (recO)
 (*Escherichia coli*) 62.9 77.6 589 HI0568 584850 584159 DOD protein (dod)
 (*Serratia marcescens*) 81.4 93.3 210 HI0062 65230 65664 dosage-dependent dnaK
 suppressor protein (dksA) (*Escherichia coli*) 73.9 83.8 142 HI0948 1005798
 1004986 lormamidopyrimidine-DNA glycosylase (lpg) (*Escherichia coli*) 57.8 74.7
 269 HI0584 602405 600519 glucose inhibited division protein (gidA)
 (*Escherichia coli*) 76.1 87.3 627 HI0488 506816 506208 glucose inhibited
 division protein (gidB) (*Escherichia coli*) 64.0 78.0 200 HI0982 1037496
 1037792 Hin recombinational enhancer binding protein (lis) (*Escherichia coli*)
 81.6 92.9 97 HI0514 528338 527565 Hinell endonuclease (Hinell) (*Haemophilus*
influenzae) 98.4 98.4 258 HI1397 1491189 1490263 HindIII modification
 methyltransferase (hindIIIM) (*Haemophilus influenzae*) 99.4 99.4 309 HI1398
 1492072 1491173 HindIII restriction endonuclease (hindIIIR) (*Haemophilus*
influenzae) 99.7 99.7 300 HI0315 345085 344474 Holiday junction DNA helicase
 (ruvA) (*Escherichia coli*) 58.8 79.9 203 HI0314 344483 343459 Holiday junction
 DNA helicase (ruvB) (*Escherichia coli*) 80.9 90.0 330 HI0678 719084 718180
 integrase/recombinase protein (xerC) (*Escherichia coli*) 58.0 74.0 293 HI1316
 1391102 1391389 integration host factor alpha-subunit (himA) (*Escherichia*
coli) 63.8 83.0 94 HI1224 1291400 1291581 integration host factor beta-subunit
 (IHF-beta) (himD) (*Escherichia coli*) 56.5 77.2 92 HI0404 422970 423539
 methylated-DNA--protein-cysteine methyltransferase (dall) (*Bacillus* 40.1 61.7
 163 *subtilis*) HI0671 713369 713806 mioC protein (mioC) (*Escherichia coli*)
 53.6 71.5 144 HI1043 1104813 1105724 modification methylase HgiDI (MHgiDI)
 (*Herpesovirus parvovirus*) 56.4 70.5 297 HI0515 529891 528338 modification
 methylase HincII (hincIIM) (*Haemophilus influenzae*) 98.2 96.6 502 HI0912
 963611 964312 mutator mutT (AT-GC transversion) (*Escherichia coli*) 48.8 72.0
 125 HI0193 206098 206688 negative modulator of initiation of replication
 (seqA) (*Escherichia coli*) 53.1 71.8 177 HI0548 568202 567879 primosomal
 protein n precursor (priB) (*Escherichia coli*) 57.4 75.2 101 HI0341 367532
 365343 primosomal protein replication factor (priA) (*Escherichia coli*) 52.3
 70.2 729 HI0389 406402 408321 probable ATP-dependent helicase (dinG)
 (*Escherichia coli*) 32.2 51.1 860 HI0993 1054243 1053119 recF protein (recF)
 (*Escherichia coli*) 57.0 75.8 356 HI0334 358532 359239 recO protein (recO)
 (*Escherichia coli*) 64.6 75.5 226 HI0502 621957 620896 recombinase (recA)
 (*Haemophilus influenzae*) 100.0 100.0 354 HI0061 64971 62573 recombination
 protein (rec2) (*Haemophilus influenzae*) 99.9 99.9 800 HI0445 464118 464717
 recR protein (recR) (*Escherichia coli*) 74.9 88.4 199 HI0601 620735 620358
 regulatory protein (recX) (*Pseudomonas fluorescens*) 26.6 50.4 117 HI0651
 694862 692768 rep helicase (rep) (*Escherichia coli*) 66.9 82.7 669 HI1232
 1299240 1297177 replication protein (dnaX) (*Escherichia coli*) 52.9 69.8 643
 HI1580 1641089 1642600 replicative DNA helicase (dnaB) (*Escherichia coli*) 68.6
 82.8 482 HI1042 1103812 1104813 restriction enzyme (hgiDIR) (*Herpesovirus*
gigantisus) 44.2 83.9 350 HI1175 1241423 1242574 S-adenosylmethionine
 synthetase 2 (metX) (*Escherichia coli*) 82.3 91.7 383 HI1429 1512163 1511552
 shufflon-specific DNA recombinase (rci) (*Escherichia coli*) 31.1 55.5 259
 HI0251 281830 282333 single-stranded DNA binding protein (sab) (*Haemophilus*
influenzae) 95.8 98.2 168 HI1576 1639113 1638016 site-specific recombinase
 (rcd) (*Escherichia coli*) 36.3 57.0 268 HI1368 1450325 1452928 topoisomerase I
 (topA) (*Escherichia coli*) 72.0 84.3 855 HI0446 464736 466688 topoisomerase
 III (tpoB) (*Escherichia coli*) 65.9 79.4 645 HI1535 1598641 1601881

topoisomerase IV subunit A (parC) (Escherichia coli) 71.4 65.4 727 HI1534
 1597676 1599571 topoisomerase IV subunit B (parE) (Escherichia coli) 76.5 88.6
 630 HI1261 1331575 1335011 transcription-repair coupling factor (trcF) (mld)
 (Escherichia coli) 64.3 82.7 1134 HI0217 232884 234038 type I restriction
 enzyme ecokI specificity protein (hsdS) (Escherichia coli) 36.1 58.6 394
 HI0216 231281 232797 type I restriction enzyme ECOR124/3 I M protein (hsdM)
 (Escherichia coli) 81.2 89.3 512 HI1290 1368549 1367223 type I restriction
 enzyme ECOR124/3 I M protein (hsdM) (Escherichia coli) 30.4 53.7 332 HI1288
 1365756 1362592 type I restriction enzyme ECOR124/3 R protein (hsdR)
 (Escherichia coli) 30.4 52.7 991 HI1059 1123091 1121206 type III
 restriction-modification ECOP15 enzyme (mod) (Escherichia coli) 36.5 55.5 384
 HI0018 18087 18743 uracil DNA glycosylase (ung) (Escherichia coli) 70.2 79.5
 215 HI0311 342051 342941 aprB protein (merD) (Escherichia coli) 68.9 84.8 296
 Degradation of DNA HI1698 1756680 1759312 endonuclease III (nth) (Escherichia
 coli) 83.4 91.9 211 HI0250 278526 281829 excinuclease ABC subunit A (uvrA)
 (Escherichia coli) 81.2 91.0 940 HI1250 1323924 1321888 excinuclease ABC
 subunit B (uvrB) (Escherichia coli) 78.0 87.7 669 HI0057 68893 67067
 excinuclease ABC subunit C (uvrC) (Escherichia coli) 65.9 80.0 588 HI0380
 1471626 1473044 exodeoxyribonuclease I (abcB) (Escherichia coli) 57.5 74.9 462
 HI1324 1395898 1399530 exodeoxyribonuclease V (recB) (Escherichia coli) 37.1
 58.2 1165 HI0944 998895 1002257 exodeoxyribonuclease V (recC) (Escherichia
 coli) 40.1 61.2 1114 HI1325 1399533 1401452 exodeoxyribonuclease V (recD)
 (Escherichia coli) 40.0 59.3 570 HI0041 43872 43072 exonuclease III (xthA)
 (Escherichia coli) 71.9 83.9 267 HI0399 417972 419288 exonuclease VII, large
 subunit (xseA) (Escherichia coli) 57.8 74.4 437 HI1217 1280795 1282519
 single-stranded-DNA-specific exonuclease (recJ) (Escherichia coli) 59.2 77.3
 554 Transcription RNA synthesis, modification and DNA transcription HI0618
 647724 650492 ATP-dependent helicase HEPA (hepA) (Escherichia coli) 53.6 73.6
 968 HI0424 444751 443435 ATP-dependent RNA helicase (srmB) (Escherichia coli)
 39.8 60.9 448 HI0232 260978 262816 ATP-dependent RNA helicase DEAD (dead)

US-PAT-NO: 6335170

DOCUMENT-IDENTIFIER: US 6335170 B1

TITLE: Gene expression in bladder tumors

DATE-ISSUED: January 1, 2002

INVENTOR-INFORMATION:

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US-CL-CURRENT: 435/6,435/91.1 ,435/91.2 ,536/23.1 ,536/24.3 ,536/24.31 ,536/24.33

ABSTRACT:

Methods for analyzing tumor cells, particularly bladder tumor cells employ gene expression analysis of samples. Gene expression patterns are formed and compared to reference patterns. Alternatively gene expression patterns are manipulated to exclude genes which are expressed in contaminating cell populations. Another alternative employs subtraction of the expression of genes which are expressed in contaminating cell types. These methods provide improved accuracy as well as alternative basis for analysis from diagnostic and prognostic tools currently available.

21 Claims, 24 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 15

DATE FILED: February 22, 2000

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DETL:

M27891_at Human cystatin C (CST3) gene 1363 943 1769 1850 835 827
M27968_s_at Human basic fibroblast growth factor (FGF) "mRNA," complete cds 20
20 20 24 20 34 M28130_ma1_s.sub.--at Human interleukin 8 (IL8) "gene,"
complete cds 54 20 20 20 20 104 M28170_at Human Human cell surface protein
CD19 (CD19) "gene," complete cds 20 20 20 20 20 20 M28209_at Homo sapiens
GTP-binding protein (RAB1) "mRNA," complete cds 321 175 347 175 58 328
M28210_at Homo sapiens GTP-binding protein (RAB3A) "mRNA," complete cds 20 20
20 20 20 20 M28211_at Homo GTP-binding protein (RAB4) "mRNA," complete cds 85
20 20 125 56 149 M28212_at Homo GTP-binding protein (RAB6) "mRNA," complete
cds 48 20 56 84 258 112 M28213_s_at Homo sapiens GTP-binding protein (RAB2)
"mRNA," complete cds 241 156 252 269 118 112 M28214_at Homo sapiens
GTP-binding protein (RAB3B) "mRNA," complete cds 20 20 20 20 20 20 M28215_at
Homo sapiens GTP-binding protein (RAB5) "mRNA," complete cds 68 20 46 125 66
41 M28219_at Homo sapiens low density lipoprotein receptor (FH 10 mutant
causing familial hypercholesterolemia) mRNA, 3' end. 55 98 20 125 66 41
M28249_at Human very late antigen-2 (VLA-2)/collagen receptor alpha-2 subunit
"mRNA," complete cds 20 37 32 78 53 20 M28439_at Human keratin type 16 gene
20 20 20 23 20 20 M28585_f_at Human leukocyte interferon-alpha "mRNA,"
complete "cds," clone pIFN105 20 20 28 20 21 26 M28713_at Homo sapiens
NADH-cytochrome b5 reductase (b5R) gene 241 324 96 204 435 152 M28825_at
Human thymocyte antigen CD1a "mRNA," complete cds 20 20 20 53 82 20

M28826_at Human thymocyte antigen CD1b "mRNA," complete cds 20 20 23 35 20 40
M28827_at Human thymocyte antigen CD1c "mRNA," complete cds 50 20 20 20 39 20
M28879_at Human granzyme B (CTLA-1) "gene," complete cds 25 122 136 89 171 77
M28882_s_at Human MUC18 glycoprotein "mRNA," complete cds 85 95 33 20 446 150
M28983_at Homo sapiens interleukin 1 alpha (IL 1) "mRNA," complete cds 74 44
57 50 140 51 M29037_s_at Human 17 beta-hydroxysteroid dehydrogenase (17BHSDI)
"gene," exons "1-5," complete cds 26 20 20 20 485 77 M29064_at Human hnRNP B1
protein mRNA 353 270 694 323 132 252 M29194_at Human triglyceride lipase
gene 20 41 20 20 148 109 M29204_at Human DNA-binding factor "mRNA," complete
cds 55 20 123 32 85 99 M29273_at Human myelin-associated glycoprotein (MAG)
"mRNA," complete cds 128 36 20 242 386 550 M29277_at 208 89 403 198 520
287 M29277_s_at Human isolate JuSo MUC18 glycoprotein mRNA (3' "variant),"
complete cds 20 20 20 20 20 20 M29335_at 20 20 20 20 1043 217 M29335_s_at
Human NHC class II DO-alpha "mRNA," partial cds 20 20 20 20 20 20
M29386_s_at Human prolactin "mRNA," 3' end 21 28 98 61 259 20 M29458_at
Human carbonic anhydrase III gene 20 20 20 38 20 20 M29474_at Human
recombination activating protein (RAG-1) "gene," complete cds 20 23 20 20 20
20 M29536_at Human translational initiation factor 2 beta subunit
(eIF-2-beta) "mRNA," complete cds 238 207 312 213 140 78 M29540_at Human
carcinoembryonic antigen mRNA "(CEA)," complete cds 483 20 116 20 108 20
M29550_at Human calcineurin A1 "mRNA," complete cds 21 80 134 51 49 20
M29551_at Human calcineurin A2 "mRNA," complete cds 21 31 20 27 20 20
M29580_at Human zinc-finger protein 7 (ZFP7) "mRNA," complete cds 20 20 20 23
20 20 M29581_at Human zinc-finger protein 8 (ZFP8) "mRNA," 3' end 98 65 161
112 124 111 M29610_at 42 22 31 20 20 20 M29610_s_at Human glycoporphin E
"mRNA," complete cds 20 27 20 31 126 41 M29696_at Human interleukin-7
receptor (IL-7) "mRNA," complete cds 246 251 192 178 387 457 M29874_s_at
Human cytochrome P450-IIB (hIIB1) "mRNA," complete cds 185 20 20 20 20 20
M29877_at Human "alpha-L-fucosidase," complete cds 181 457 1112 462 416 275
M29927_at Human ornithine aminotransferase gene 147 49 20 20 20 20
M29932_s_at Human beta030adrenergic receptor gene 89 137 328 136 190 86
M29960_at Human steroid receptor (TR2011) "mRNA," complete cds 68 215 173 146
142 130 M29971_at Human 6-O-methylguanine-DNA methyltransferase (MGMT)
"mRNA," complete cds 51 165 20 136 89 232 M29994_s_at Human alpha-I spectrin
"gene," exon 12 /gb=M29994 /ntype=DNA /annot=exon 20 56 62 32 20 37
M30135_at Human P40 T-cell and mast cell growth factor (hP40) "gene," complete
cds 20 20 20 20 20 20 M30185_at Human cholesteryl ester transfer protein
"mRNA," complete cds 20 20 20 20 20 20 M30257_s_at Human vascular cell
adhesion molecule 1 "mRNA," complete cds 59 85 59 45 39 29 M30269_at Human
ridogen "mRNA," complete cds 82 20 28 29 20 90 M30448_s_at 239 357 738 687
536 273 M30496_at Human ubiquitin carboxyl-terminal hydrolase (PGP "9.5,"
UCH-L3) isozyme L3 "mRNA," complete cds 33 44 57 44 26 20 M30607_s_at Human
zinc finger protein Y-linked (ZFY) "mRNA," complete cds 30 21 127 70 113 25
M30625_s_at Human dopamine D2 "receptor," "mRNA," complete cds 20 20 20 20 70
20 M30703_s_at Human amphiregulin (AR) gene 160 20 20 20 49 20 M30773_at
Human calcineurin B "mRNA," complete cds 20 20 20 20 20 20 M30818_at Human
interferon-induced cellular resistance mediator protein (MxB) "mRNA," complete
cds 63 98 52 40 333 204 M30838_at Human pulmonary surfactant apoprotein
(PSAP) "gene," complete cds 50 56 28 32 97 40 M30984_at human T-cell
receptor Ti rearranged gamma-chain mRNA V-J-C "region," complete cds 95 75
171 117 149 59 M30938_at Human Ku (p70/p80) subunit "mRNA," complete cds 121
93 507 196 45 35 M31013_at Human nonmuscle myosin heavy chain (NMHC) "mRNA,"
3' end 274 175 792 266 232 258 M31153_at Human steroid 17-alpha-hydroxylase

gene 20 20 20 20 20 20 M31158_at Human cAMP-dependent protein kinase subunit
 RIII-beta "mRNA," complete cds 51 20 35 28 20 20 M31165_at Human tumor
 necrosis factor-inducible (TSG-6) mRNA "fragment," adhesion receptor CD44
 putative CDS 20 20 20 20 60 20 M31166_at Human tumor necrosis
 factor-inducible (TSG-14) "mRNA," complete cds 36 20 20 20 20 20 M31169_s_at
 Human propionyl-CoA carboxylase beta-subunit (beta-PCC) "gene," partial cds
 (mutant delta-ATC). /gb=M31169 /ntype=DNA /annot=CD 30 29 20 67 20 66
 M31210_at Human endothelial differentiation protein (edg-1) gene "mRNA,"
 complete cds 35 49 33 20 20 20 M31211_s_at Human myosin light chain 1 show a
 (MLC1sa) "mRNA," complete cds 25 20 20 20 26 71 M31241_s_at Human complement
 receptor 1 (CR1) gene 20 40 20 26 20 20 M31303_ma1_at Human oncoprotein 18
 (Op18) gene, complete cds. 271 274 373 245 752 751 M31328_at Human guanine
 nucleotide-binding protein beta-3 subunit "mRNA," complete cds 182 112 211
 140 182 255 M31423_s_at Human cerebellar-degeneration-related antigen (CDR34)
 "gene," complete cds 20 20 20 27 92 20 M31516_s_at Human decay-accelerating
 factor "mRNA," complete cds 49 20 45 62 20 20 M31520_at Human ribosomal
 protein S24 mRNA 1876 2526 3539 2479 885 1027 M31520_ma1_at 20 20 36 55 20
 20 M31520_ma1_s_at Human ribosomal protein S24 mRNA 2242 7095 5080 4489 1497
 1572 M31523_at Human transcription factor (E2A) "mRNA," complete cds 20 39
 40 106 205 120 M31525_at Human NHC class II lymphocyte antigen (HLA-DNA)
 "gene," complete cds 314 176 281 263 580 522 M31551_s_at Human urokinase
 inhibitor (PAI-2) gene 219 20 20 41 59 20 M31606_at Human phosphorylase
 kinase (PSK-C3) "mRNA," complete cds 20

DETL:

20 20 29 25 20 20 U78180_at Human sodium channel 2 (hBNaC2) "mRNA,"
 alternatively "spliced," complete cds 20 20 20 20 42 20 U78190_ma1_at Human
 GTP cyclohydrolase I feedback regulatory protein gene, complete cds. 20 24 20
 20 147 107 U78313_at Human myogenic repressor I-mf (MDFI) "mRNA," complete
 cds 37 54 80 87 85 20 U78521_at Homo sapiens immunophilin homolog ARA9
 "mRNA," complete cds 296 294 313 290 412 472 U78524_at Human Gu binding
 protein "mRNA," partial cds. 147 143 129 152 31 229 U78525_at Human
 eukaryotic translation initiation factor (eIF3) "mRNA," complete cds 74 172
 162 146 176 215 U78551_at Homo sapiens gallbladder mucin MUC5B "mRNA,"
 partial cds 35 20 20 20 20 20 U78556_at Human cisplatin resistance associated
 alpha protein (hCRA alpha) "mRNA," complete cds 104 104 112 112 239 178
 U78575_at Human 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha
 "mRNA," clone "PIP5K1a1," complete cds 92 44 117 74 189 132 U78628_at Human
 leukemia inhibitory factor receptor "mRNA," 5' untranslated region. /gb=U78628
 /ntype=RNA 28 51 39 40 62 54 U78678_at Human thioredoxin "mRNA," nuclear gene
 encoding mitochondrial "protein," complete cds 215 319 217 236 521 546
 U78722_at Homo sapiens zinc finger protein 165 (Zpf165) "mRNA," complete cds.
 20 20 20 20 91 58 U78735_at Human ABC3 "mRNA," complete cds. 39 40 29 34 97
 53 U78793_at Human folate receptor alpha (hFR) "mRNA," partial cds.
 /gb=U78793 /ntype=RNA 118 115 90 75 147 30 U78798_at Human TNF receptor
 associated factor 6 (TRAF6) "mRNA," complete cds. 148 96 52 91 152 61
 U78876_at Human MEK kinase 3 "mRNA," complet cds 20 20 20 20 20 20
 U79115_s_at Human death adaptor molecule RAIDD (RAIDD) "mRNA," complete cds.
 20 20 20 20 41 46 U79241_at Human clone 23759 "mRNA," partial cds. 20 97 20
 20 20 53 U79242_at Human clone 23560 mRNA sequence 20 45 20 20 51 42
 U79245_at Human clone 23586 mRNA sequence 25 20 20 20 20 20 U79246_at Human
 clone 23799 mRNA sequence 20 20 20 20 20 20 U79247_at Human clone 23599 mRNA
 sequence 20 20 20 20 20 20 U79248_at Human clone 23826 mRNA sequence 20 20

20 20 20 20 U79249_at Human clone 23839 mRNA sequence 20 20 20 20 20 20
 U79251_at Human clone 23878 mRNA sequence 34 20 31 21 20 20 U79252_at Human
 clone 23679 "mRNA," complete cds. 82 76 82 78 143 151 U79253_at Human clone
 23893 "mRNA," complete cds. 20 20 20 26 99 25 U79254_at Human clone 23693
 mRNA sequence 165 188 269 298 82 87 U79255_at Human X11 protein "mRNA,"
 partial cds. 67 25 20 20 225 21 U79256_at Human clone 23719 mRNA sequence
 35 20 20 26 68 74 U79257_at Human clone 23932 mRNA sequence 20 20 21 20 20
 20 U79258_at Human clone 23732 "mRNA," partial cds. 27 20 34 20 70 40
 U79259_at Human clone 23945 "mRNA," complete cds. 89 29 138 117 20 20
 U79260_at Human clone 23745 "mRNA," complete cds. 112 84 135 86 143 163
 U79261_s_at Human clone 23959 "mRNA," partial cds. 20 20 20 20 25 20
 U79262_at Human deoxyhypusine synthase "mRNA," complete cds. 106 87 151 141
 83 212 U79263_at Human clone 23760 "mRNA," partial cds. 20 24 20 20 20 20
 U79265_at Human clone 23614 mRNA sequence 20 57 20 28 20 20 U79266_at Human
 clone 23627 "mRNA," complete cds. 178 148 104 98 150 224 U79267_at Human
 clone 23840 "mRNA," partial cds. 110 70 66 90 72 39 U79270_at Human clone
 23707 "mRNA," partial cds. 20 20 29 30 20 20 U79271_at Human clones 23920
 and 23921 mRNA sequence 20 32 20 20 20 53 U79272_at Human clone 23720 mRNA
 sequence 20 26 20 20 20 20 U79273_at Human clone 23933 mRNA sequence 22 45
 30 20 20 20 U79274_at Human clone 23733 "mRNA," complete cds. 51 62 36 27 93
 76 U79275_at Human clone 23947 "mRNA," partial cds. 194 138 132 103 165 61
 U79277_at Human clone 23548 mRNA sequence 20 20 20 20 20 37 U79280_at Human
 clone 23575 "mRNA," partial cds. 93 39 42 56 226 105 U79282_at Human clone
 23801 mRNA sequence 20 20 22 30 20 48 U79285_at Human clone 23828 mRNA
 sequence 39 56 20 42 99 157 U79286_at Human arginine methyltransferase
 "mRNA," complete cds. 20 20 20 20 20 20 U79287_at Human clone 23867 mRNA
 sequence 88 135 177 233 98 147 U79288_at Human clone 23682 mRNA sequence 73
 27 47 20 39 20 U79289_at Human clone 23695 mRNA sequence 20 20 20 20 20 52
 U79290_at Human clone 23908 mRNA sequence 20 20 37 21 20 24 U79291_at Human
 clone 23721 mRNA sequence 50 20 31 25 20 48 U79293_at Human clone 23948 mRNA
 sequence 20 20 20 20 24 20 U79294_at Human clone 23748 "mRNA," complete cds.
 370 417 294 256 286 241 U79295_at Human clone 23961 mRNA sequence 44 20 20
 20 164 20 U79296_at Human dihydrolipoamide acetyl transferase "mRNA," partial
 cds. 31 20 31 23 141 60 U79297_at Human clone 23589 mRNA sequence 60 38 55
 61 20 20 U79298_at Human clone 23803 "mRNA," partial cds. 72 20 28 21 57 20
 U79299_at Human neuronal olfactomedin-related ER localized protein "mRNA,"
 partial cds. 20 35 20 20 117 232 U79300_at Human clone 23629 mRNA sequence
 20 20 20 20 102 24 U79301_at Human clone 23842 mRNA sequence 20 20 20 20 42
 20 U79302_at Human clone 23855 "mRNA," partial cds. 20 20 20 20 63 28
 U79303_at Human clone 23882 "mRNA," complete cds. 158 20 163 177 55 175
 U79304_at Human clone 23909 "mRNA," partial cds. 20 20 20 20 99 20 U79526_at
 Human orphan G-protein coupled receptor Dez isoform a "mRNA," complete cds 20
 20 20 20 20 20 U79528_s_at Human SR31747 binding protein 1 "mRNA," complete
 cds 160 195 494 308 399 319 U79667_s_at Human alpha1A-voltage-dependent
 calcium channel "mRNA," splice form "VI-1-V2-GGCAG," partial cds 20 20 20 20
 20 20 U79716_at Human reelin (RELN) "mRNA," complete cds 43 20 20 28 58 20
 U79718_at Human endonuclease III homolog 1 (OCTS3) "mRNA," complete cds. 20 20
 24 22 35 20 U79725_at Human A33 antigen precursor "mRNA," complete cds 20 48
 42 32 112 49 U79734_at Human huntingtin interacting protein (HIP1) "mRNA,"
 complete cds. 20 20 20 20 20 20 U79751_at Human basic-leucine zipper nuclear
 factor (JEM-1) "mRNA," complete cds. /gb=U79751 /ntype=RNA 20 20 20 20 20 20
 U80017_ma1_at Human basic transcription factor 2 prr (btf2p44) gene, partial
 cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron 20

20 20 20 20 20 U80017_ma2_at Human basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron 20 20 20 20 20 20 U80017_ma3_at Human basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron 71 34 82 73 41 39 U80034_at Human mitochondrial intermediate peptidase precursor (MIPEP) "mRNA," mitochondrial gene encoding mitochondrial "protein," complete 20 20 20 20 20 20 U80040_at Human nuclear aconitase "mRNA," encoding mitochondrial "protein," complete cds 120 95 212 200 168 184 U80073_at Human tip associating protein (TAP) "mRNA," complete cds. /gb=U80073 /ntype=RNA 37 20 96 84 20 85 U80184_ma1_at Homo sapiens FLII gene, complete cds. 87 45 63 157 20 20

DETL:

X97074_at H. sapiens mRNA for clathrin-associated protein 247 148 113 128 121 231 X97160_ma1_at H. sapiens TFE3 gene, exons 1,2,3 (and joined CDS). 101 91 69 75 140 140 X97198_at H. sapiens mRNA for receptor phosphate PCP-2 24 43 80 84 152 53 X97230_f_at H. sapiens mRNA for NK "receptor," clone library 4M1#6 46 29 96 20 20 67 X97249_at H. sapiens mRNA for leucine-rich primary response protein 1 41 40 43 26 20 68 X97261_at H. sapiens mRNA for metallothionein isoform 1R 40 20 20 27 55 45 X97261_r_at H. sapiens mRNA for metallothionein isoform 1R 20 20 20 20 20 20 X97267_ma1_s_at H. sapiens LPAP gene 20 20 20 20 20 199 X97301_at H. sapiens mRNA for Ptg-11 protein. /gb=X97301 /ntype=RNA 20 20 20 20 30 20 X97302_at H. sapiens mRNA for Ptg-1 protein. /gb=X97302 /ntype=RNA 90 100 108 79 217 145 X97303_at H. sapiens mRNA for Ptg-12 protein. /gb=X97303 /ntype=RNA 20 20 20 20 20 55 X97324_at H. sapiens mRNA for adipophilin. /gb=X97324 /ntype=RNA 20 20 141 65 20 186 X97335_at H. sapiens mRNA for kinase A anchor protein 20 20 25 45 20 20 X97444_f_at H. sapiens mRNA for transmembrane protein Tmp21-Ilex. /gb=X97444 /ntype=RNA 50 20 93 80 20 40 X97544_at H. sapiens mRNA for TIM17 preprotein translocase 24 36 50 49 46 28 X97630_at H. sapiens mRNA for serine/threonine protein kinase EMK 20 21 21 20 62 20 X97671_at H. sapiens mRNA for erythropoietin receptor 20 20 20 20 32 20 X97674_at H. sapiens mRNA for transcriptional intermediary factor 2 20 20 20 20 20 20 X97675_ma1_at H. sapiens mRNA for pfakophilin 2a and b. 20 20 20 20 20 20 X97748_s_at H. sapiens PTX3 gene promoter region. /gb=X97748 /ntype=DNA /annot=mRNA 20 20 20 20 31 20 X97795_at H. sapiens mRNA homologous to S. cerevisiae RAD54 20 20 20 20 20 20 X98001_at H. sapiens mRNA for geranylgeranyl transferase II 70 45 48 42 20 20 X98085_at H. sapiens mRNA for tenascin-R 225 202 186 215 173 226 X98172_at H. sapiens mRNA for MACH-alpha-1 protein 45 42 65 43 64 45 X98176_at H. sapiens mRNA for MACH-beta-1 protein. /gb=X98176 /ntype=RNA 24 30 22 35 20 20 X98178_s_at H. sapiens mRNA for MACH-beta-4 protein. /gb=X98178 /ntype=RNA 20 20 31 25 20 20 X98206_at H. sapiens mRNA for UV-B repressed "sequence," HUR 8 /gb=X98206 /ntype=RNA 20 20 20 20 20 20 X98225_at H. sapiens mRNA for gastrin-binding protein. /gb=X98225 /ntype=RNA 20 20 20 20 20 20 X98248_ma1_at H. sapiens mRNA for sortilin. 46 22 41 44 23 71 X98253_at H. sapiens ZNF183 gene. /gb=X98253 /ntype=RNA 23 62 114 87 85 84 X98258_at H. sapiens mRNA for M-phase "phosphoprotein," mpp9 20 20 20 20 26 35 X98260_at H. sapiens mRNA for M-phase "phosphoprotein," mpp11 43 35 67 42 20 41 X98261_at H. sapiens mRNA for M-phase "phosphoprotein," mpp5 81 55 91 79 80 118 X98263_at H. sapiens mRNA for M-phase "phosphoprotein," mpp6 89 56 103 64 170 77 X98266_cds2_at H. sapiens mRNA for ligase like protein, X-1. 20 20 20 20 20 20 X98296_at H. sapiens mRNA for ubiquitin hydrolase 84 169 143 170 176 51 X98307_at H. sapiens mRNA for UV-B repressed "sequence,"

HUR 7 43 20 21 20 104 20 X98311_at H. sapiens mRNA for carcinoembryonic
 "antigen," CGM2 154 113 20 20 20 20 X98330_at H. sapiens mRNA for ryanodine
 receptor 2 20 20 20 20 59 23 X98337_s_at H. sapiens mRNA for complement
 factor H-related protein 4 39 26 46 33 97 20 X98411_at H. sapiens mRNA for
 myosin-IE 105 97 63 76 90 80 X98482_at H. sapiens TNNT2 gene exon 11
 /gb=X98482 /ntype=DNA /annot=mRNA 20 20 20 20 181 38 X98482_r_at H. sapiens
 TNNT2 gene exon 11 /gb=X98482 /ntype=DNA /annot=mRNA 3885 2448 5047 2490 20
 20 X98507_at H. sapiens mRNA for myosin-I beta 23 45 38 37 123 72
 X98534_s_at H. sapiens VASP "gene," exons 4 to 13 48 180 126 156 20 75
 X98743_at H. sapiens mRNA for RNA helicase (Myc-regulated dead box protein) 84
 58 105 82 58 106 X98801_at H. sapiens mRNA for dynactin 69 87 90 81 248 133
 X98833_ma1_at H. sapiens mRNA for zinc finger protein, Hsa1. 20 20 20 20 63
 20 X98834_ma1_at H. sapiens mRNA for zinc finger protein, Hsa2. 20 20 34 29
 62 20 X99050_ma1_at H. sapiens mRNA; UV Radiation Resistance Associated Gene
 37 53 24 31 48 74 X99076_ma1_at H. sapiens NRG1 gene, exons 2.3 & 4 (joined
 CDS). 20 20 20 20 20 20 X99101_at H. sapiens mRNA for estrogen receptor. 30
 38 31 22 50 20 X99133_at H. sapiens NGAL gene 384 1351 20 20 420 78
 X99140_at H. sapiens mRNA for hair "keratin," hHb5 20 22 20 20 68 20
 X99141_at H. sapiens mRNA for hair "keratin," hHb3 105 124 85 65 283 224
 X99142_at H. sapiens mRNA for hair "keratin," hHb6 135 20 75 65 35 82
 X99209_at H. sapiens mRNA for arginine methyltransferase 82 170 226 110 201
 156 X99226_at H. sapiens mRNA for FAA protein 20 51 20 28 20 40 X99268_at
 H. sapiens mRNA for B-HLH DNA binding protein 20 20 20 20 20 20
 X99296_xpt1_at H. sapiens RD gene (5' partial) and G11a gene (5' partial). 20
 20 20 20 73 20 X99325_at H. sapiens mRNA for Ste20-like kinase 63 50 145
 100 100 77 X99350_ma1_at H. sapiens HFH4 gene, exon 1 and joined CDS. 20 20
 20 20 122 20 X99374_s_at H. sapiens mRNA for fertilin beta 20 20 20 20 20 20
 X99393_s_at H. sapiens CMKBR5 "gene," non-functional mutant 20 20 34 20 89 33
 X99459_at H. sapiens mRNA for sigma 3B protein 141 176 148 155 199 215
 X99479_f_at H. sapiens mRNA for NK "receptor," clone 12.11C 20 20 20 20 73 72
 X99584_at H. sapiens mRNA for SMT3A protein 27 28 28 27 49 20 X99585_at H.
 sapiens mRNA for SMT3B protein 206 93 185 210 115 288 X99586_s_at H. sapiens
 mRNA for SMT3C protein 20 20 20 20 20 20 X99656_at H. sapiens mRNA for
 protein containing SH3 "domain," SH3GL1 21 20 20 20 30 20 X99657_at H.
 sapiens mRNA for protein containing SH3 "domain," SH3GL2 20 20 20 20 20 20
 X99664_at H. sapiens mRNA for protein containing SH3 "domain," SH3GL3 31 20
 39 29 20 71 X99687_at H. sapiens mRNA for methyl-CpG-binding protein "2,"
 intron 2 /gb=X99687 /ntype=RNA 51 23 46 31 85 38 X99688_at H. sapiens mRNA
 from TYL gene 242 355 283 213 543 447 X99699_at H. sapiens mRNA for XIAP
 associated factor-1 24 38 40 20 23 43 X99720_ma1_at H. sapiens TPRC gene.
 20 20 20 42 71 40 X99728_at H. sapiens NDUFV3 "gene," exon 3 /gb=X99726
 /ntype=DNA /annot=exon 109 110 87 116 165 210 X99802_at H. sapiens mRNA for
 ZYG homologue 20 20 20 20 20 20 X99886_s_at H. sapiens MCP-2 gene 40 20 20
 20 75 20 X99894_at H. sapiens mRNA coding for insulin promoter factor 1 20 20
 20 20 20 20 X99897_s_at H. sapiens mRNA for P/Q-type calcium channel alpha1
 subunit 20 20 20 20 20 20 X99920_at H. sapiens mRNA for S100 calcium-binding
 protein A13 145 176 108 131 20 51 X99947_at H. sapiens mRNA dynein-related
 protein 32 20 20 20 58 38 X99961_at H. sapiens mRNA for novel protein.
 /gb=X99961 /ntype=RNA 20

DETL:

20 20 20 20 20 20 Y09561_at H. sapiens mRNA for P2X7 receptor 27 20 20 20
 20 20 Y09615_at H. sapiens mRNA for mitochondrial transcription termination

factor 20 25 20 20 20 20 Y09616_at H. sapiens mRNA for putative
 carboxylesterase 121 92 143 96 135 159 Y09836_at H. sapiens mRNA for 3'UTR
 of unknown protein 62 35 20 20 64 20 Y09858_at H. sapiens mRN for unknown
 protein 20 30 27 24 52 38 Y09912_ma1_at H. sapiens AP-2 beta gene. 20 20
 20 20 20 20 Y09943_s_at H. sapiens mRNA for NGF-inducible PC3
 anti-proliferative protein 20 20 20 20 20 20 Y09980_ma4_at H. sapiens HOXD3
 gene. 20 27 27 20 56 20 Y10032_at H. sapiens mRNA for putative
 serine/threonine protein kinase 130 28 20 26 76 107 Y10055_at H. sapiens
 mRNA for phosphoinositide 3-kinase 20 20 20 20 149 85 Y10141_s_at H. sapiens
 DAT1 "gene," "partial," VNTR. /gb=Y10141 /ntype=DNA /annot=CDS 20 20 133 24
 231 143 Y10202_at H. sapiens mRNA for CD207 protein. /gb=Y10202 /ntype=RNA 20
 20 20 20 20 24 Y10204_at H. sapiens mRNA for CD77 protein. /gb=Y10204
 /ntype=RNA 20 24 20 20 20 20 Y10205_at H. sapiens mRNA for CD88 protein.
 /gb=Y10205 /ntype=RNA 20 20 20 20 20 20 Y10207_at H. sapiens mRNA for CD171
 protein. /gb=Y10207 /ntype=RNA 57 90 27 20 135 211 Y10209_at H. sapiens mRNA
 for CD30L protein. /gb=Y10209 /ntype=RNA 20 20 20 20 20 20 Y10210_at Y.
 sapiens mRNA for CD22 protein. /gb=Y10210 /ntype=RNA 20 20 20 20 20 20
 Y10256_at H. sapiens mRNA for serine/threonine protein "kinase," NIK 20 20 20
 20 53 20 Y10260_at H.sapiens EYA1 gene 20 40 20 20 125 21 Y10262_s_at H.
 sapiens EYA3 gene. /gb=Y10262 /ntype=DNA /annot=CDS 20 20 66 20 112 29
 Y10275_at H. sapiens mRNA for L-3-phosphoserine phosphatase 20 20 20 20 30 20
 Y10313_at H. sapiens mRNA for nerve growth factor-incucible PC4 homologue 34
 26 26 20 95 51 Y10375_s_at H. sapiens mRNA for SIRP-alpha1 20 20 20 20 467
 139 Y10376_at H. sapiens mRNA for SIRP-beta1 106 20 33 30 20 147 Y10505_at
 H. sapiens mRNA for CD104 protein. /gb=Y10505 /ntype=RNA 20 20 20 20 20 20
 Y10506_at H. sapiens mRNA for CD110 protein. /gb=Y10506 /ntype=RNA 24 65 20
 20 59 20 Y10508_s_at H. sapiens mRNA for CD190 protein. /gb=Y10508 /ntype=RNA
 20 20 20 20 20 20 Y10510_at H. sapiens mRNA for CD67S protein. /gb=Y10510
 /ntype=RNA 20 20 20 20 47 20 Y10511_at H. sapiens mRNA for CD176 protein.
 /gb=Y10511 /ntype=RNA 23 20 20 20 20 20 Y10512_at H. sapiens mRNA for CD282
 protein. /gb=Y10512 /ntype=RNA 20 20 20 20 20 20 Y10514_s_at mNRA for CD152
 protein. /gb=Y10514 /ntype=RNA 20 26 20 31 166 55 Y10515_at H. sapiens mRNA
 for CD58 T7 protein. /gb=Y10515 /ntype=RNA 20 20 20 45 20 Y10517_at
 H.sapiens mRNA for CD108 protein. /gb=Y10517 /ntype=RNA 20 20 20 20 28 20
 Y10518_at H. sapiens mNRA for CD202 protein. /gb=Y10518 /ntype=RNA 20 20 20
 20 59 25 Y10571_at H. sapiens mRNA for dinG gen 20 20 20 20 20 22 Y10615_at
 H. sapiens CYRN2 gene. /gb=Y10615 /ntype=DNA /annot=CDS 34 20 53 34 110 63
 Y10659_at H. sapiens IL-13Ra mRNA 20 20 20 20 20 24 Y10807_s_at H. sapiens
 mRNA for arginine "methyltransferase," splice "variant," 1262 bp 87 101 558
 442 456 407 Y10812_at H. sapiens mRNA for fructose-bisphosphatase 20 20 20
 20 20 20 Y10871_at H. sapiens twist gene 110 154 116 97 279 284 Y10936_at
 H. sapiens mRNA for hypothetical protein downstream of DMPK and DMAHP 41 20
 61 35 58 40 Y11174_at H. sapiens mRNA for RP3 gene. /gb=Y11174 /ntype=RNA 20
 20 20 20 20 20 Y11180_at H. sapiens mRNA for twist "protein," partial.
 /gb=Y11180 /ntype=RNA 20 29 20 20 20 20 Y11215_at H. sapiens mRNA for SKAP55
 protein. /gb=Y11215 /ntype=RNA 34 58 55 50 20 66 Y11251_at H. sapiens mRNA
 for novel member of serine-arginine domain "protein," SRrp129 20 20 40 22 41
 20 Y11306_ma1_at Homo sapiens mRNA for hTCF-4. 67 58 63 53 20 96 Y11416_at
 H. sapiens mRNA for P73. 20 43 20 21 125 64 Y11651_at H. sapiens mRNA for
 phosphate cyclase 20 20 24 30 20 20 Y11681_at Homo sapiens mRNA for
 mitochondrial ribosomal protein S12. /gb=Y11681 /ntype=RNA 112 172 137 114 40
 154 Y11709_at H. sapiens mRNA for extracellular matrix protein collagen type
 "XIV," N-terminus. /gb=Y11709 /ntype=RNA 20 20 20 20 20 20 Y11710_ma1_at H.

sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.
 21 73 43 52 127 131 Y11897_at H. sapiens Brx gene 3'UTR. /gb=Y11897
 /ntype=RNA 66 40 57 56 159 98 Y11999_at H. sapiens mRNA for inositol
 "1,4,5-trisphosphate" 3-kinase. /gb=Y11999 /ntype=RNA 20 20 20 20 20
 Y12393_s_at H. sapiens mRNA for SRP1-like "protein," partial 20 20 88 40 20
 39 Y12394_at H. sapiens mRNA for SRP1-like protein 20 20 27 20 20 20
 Y12478_at H. sapiens mRNA for CHD5 protein 20 20 20 20 20 20 Y12556_at H.
 sapiens mRNA for AMP-activated protein kinase beta-1. /gb=Y12556 /ntype=RNA 20
 20 20 20 20 20 Y12670_at H. sapiens OB-RGRP gene. /gb=Y12670 /ntype=RNA 20
 71 165 133 20 20 Y12711_at H. sapiens mRNA for putative testosterone binding
 protein 73 48 133 153 91 65 Y12812_at H. sapiens RFXAP mRNA 20 20 20 20 20
 20 Y12856_at H. sapiens mRNA for AMP-activated protein kinase "alpha-1,"
 partial. /gb=Y12856 /ntype=RNA 41 20 22 20 105 39 Y13115_at Homo sapiens mRNA
 for serin/threonine protein kinase SAK 55 78 26 48 117 92 Y13153_at Homo
 sapiens mRNA for kynurenin 3-monooxygenase. /gb=Y13153 /ntype=RNA 32 26 24 26
 133 99 Y13247_at Homo sapiens fb19 mRNA 81 49 91 123 328 171 Y13618_at Homo
 sapiens mRNA for DFFRY "protein," abundant transcript 20 20 20 22 20 20
 Y13620_at Homo sapiens mRNA for BCL9 gene. /gb=Y13620 /ntype=RNA 20 20 20 20
 20 20 Y13896_at Homo sapiens skeletal muscle alternate 5'end of gene Kir4.2
 5'UTR. /gb=Y13896 /ntype=RNA 20 20 20 20 143 35 Y14140_at Homo sapiens G
 protein gene encoding beta 3 subunit exon 1 and promoter. /gb=Y14140
 /ntype=DNA /annot=exon 88 57 121 88 128 120 Z00010_at 20 20 20 20 38 31
 Z11502_at H. sapiens mRNA for intestine-specific annexin 20 20 20 20 66 45
 Z11518_s_at H. sapiens mRN for histidyl-tRNA synthetase 20 20 98 38 216 57
 Z11559_at H. sapiens mRNA for iron regulatory factor 38 24 28 20 20 60
 Z11685_s_at H. sapiens mRNA for RNA helicase 20 20 20 33 32 20 Z11695_at H.
 sapiens 40 kDa protein kinase related to rat ERK2 20 20 20 20 20 20
 Z11697_at Homo sapiens mRNA for HB15 27 20 25 20 87 20 Z11737_at H. sapiens
 mRNA for flavin-containing monooxygenase 4 20 20 37 20 44 20 Z11793_at H.
 sapiens mRNA for selenoprotein P 208 92 40 28 20 54 Z11850_at H. sapiens
 mRNA for somatotropin receptor 5' upstream region. /gb=Z11850 /ntype=RNA 20
 20 20 20 20 Z11899_s_at H. sapiens OTF3 mRNA encoding octamer binding
 protein 3B 68 154 191 235 94 139 Z11933_at H. sapiens mRNA for N-Oct "3,"
 "N-Oct5a," and N-Oct 5b proteins 20 20 20 20 275 20 Z12173_at H. sapiens GNS
 mRNA encoding glucosamine-6-sulphatase 20 20 20 20 20 43 Z12830_at H.
 sapiens mRNA for SSR alpha subunit 20 20 23 36 20 29 Z12962_at H. sapiens
 mRNA for homologue to yeast ribosomal protein L41 7468 11237 7087 7602 8100
 7623

DETL:

M57293_at HUMPTHRA parathyroid hormone-related pe av dif pos M57399_at
 HUMHBNF1 nerve growth factor\ (HBNF-1\) av dif pos M57399_at HUMHBNF1 nerve
 growth factor \ (HBNF-1\) av dif pos M57466_s_at HUMMHDPL MHC class II HLA-DP
 light chain av dif pos M57466_s_at, HUMMHDPL MHC class II HLA-DP light chain av
 dif pos M57710_at HUMBPIGE IgE-binding protein \ (epsilon- av dif pos
 M58378_cds1_at HUMSYN1E13 synapsin I \ (SYN1\) gene, exon av dif pos
 M58525_s_at HUMCOMTC catechol-O-methyltransferase av dif pos M58525_s_at
 HUMCOMTC catechol-O-methyltransferase av dif pos M59216_s_at UMGABRB1S5
 gamma-aminobutyric acid-A \ (GA av dif pos M59371_at HUMECK protein tyrosine
 kinase mRNA, av dif pos M59807_at HUMNK4 NK4 mRNA, :natural killer cell av
 dif pos M59830_at HUMMHSP2 MHC class III HSP70-2 gene \ (H av dif pos
 M59911_at HUMINTA3A integrin alpha-3 chain mRNA, av dif pos M80483_ma1_s_at
 HUMPP2AA protein phosphatase 2A catalyst av dif pos M60854_at HUMSRAA

ribosomal protein S16 mRNA, : av dif pos M61916_at HUMLAM101 laminin B1 chain
 mRNA, :lamin av dif pos M62403_s_at HUMIGFBP5 insulin-like growth factor bin
 av dif pos M62403_s_at HUMIGFBP5 insulin-like growth factor bin av dif pos
 M62486_at UMPRPC4SI2 C4b-binding protein gene, exon av dif pos M63256_at
 HUMCDR2AA major Yo paraneoplastic antige av dif pos M63379_at HUMTRPM2A4
 TRPM-2 protein gene, exons 7,8 av dif pos M63438_s_at HUMIGGK Ig rearranged
 gamma chain mRNA av dif pos M63438_s_at HUMIGGK Ig rearranged gamma chain
 mRNA av dif pos M63573_at HUMSCYLP secreted cyclophilin-like prot av dif pos
 M63589_at HUMSCL7 stem cell leukemia gene produc log neg M64347_at HUMFGFLR
 novel growth factor receptor m log neg M64347_at HUMFGFLR novel growth factor
 receptor m log neg M64673_at HUMHSF1 heat shock factor 1 (TCF5) m log neg
 M64716_at HUMRPS25 ribosomal protein S25 mRNA, : log neg M64992_at HUMPRO530
 prosomal protein P30-33K (pro log neg M65292_s_at HUMHAAA factor H homologue
 mRNA, :fa log neg M65292_s_at HUMHAAA factor H homologue mRNA, :fa log neg
 M69023_at HUMGGEFERA globin gene. log neg M69068_at HUMMOESIN moesin mRNA,
 :moesin :moesin log neg M69238_at HUMARNTA aryl hydrocarbon receptor nucl log
 neg M73077_at HUMGRF1A glucocorticoid receptor repres log neg M73239_s_at
 HUMSCFA1 (clone SF1) hepatocyte growt log neg M73547_at HUMPOLLA polyposis
 locus (DP1 gene) m log neg M74093_at HUMCLNC cyclin mRNA, :cyclin E1 log
 neg M74297_at HUMHOX14 homeobox 1.4 protein mRNA, :h log neg M74715_s_at
 HUMIDNAL alpha-L-iduronidas (IDUA) mR log neg M77232_ma1_at HUMRPS6B
 ribosomal protein S6 gene, com log neg M77836_at HUMP5CR pyrroline
 5-carboxylate reduct log neg M80244_at HUME16GEN E16 mRNA, log neg
 M80254_at HUMCYP cyclophilin isoform (hCyP3) log neg M80359_at HUMP78A
 protein p78 mRNA, :MAP/microt log neg M80563_at HUMCAPL CAPL protein mRNA,
 :S100 calc log neg M80563 at HUMCAPL CAPL protein mRNA, :S100 calc log neg
 M80899_at HUMAHNAKA novel protein AHNAK mRNA, part log neg M81750_at HUMMCNDA
 myeloid cell nuclear different log neg M81757_at HUMS19RP S19 ribosomal
 protein mRNA, log neg M81883_at HUMGAD67A glutamate decarboxylase (GAD6 log
 neg M83181_at HUMHTRB serotonin receptor gene, :5-h log neg M84424_at
 HUMCTSE09 cathepsin E (CTSE) gene, exo log neg M84711_at HUMFTE1A v-fos
 transfection effector log neg M85289_at HUMHSPG2B heparan sulfate
 proteoglycan log neg M86400_at HUMPHLA2 phospholipase A2 mRNA, :tyros log
 neg M86699_at HUMTTK kinase (TTK) mRNA, :TTK pro log neg M86737_at HUMHMGBP
 high mobility group box (SSRP log neg M87789_s_at HUMIGHEPAH (hybridoma
 H210) anti-hepati log neg M87789_s_at HUMIGHEPAH (hybridoma H210)
 anti-hepati log neg M90356_f_at HUMBTDF BTDF3 protein homologue gene, log neg
 M90856_at HUMGCSH gamma-glutamylcysteine synthet log neg M91670_at HUME2EP1
 ubiquitin carrier protein (E2 log neg M94856_at HUMFABPHA fatty acid binding
 protein hom log neg M94856_at HUMFABPHA fatty acid binding protein hom log
 neg M94880_f_at HUMHLAAX MHC class I (HLA-A*8001) mRN log neg M96233_s_at
 HUMGSTM4A glutathione transferase class log neg M96233_s_at HUMGSTM4A
 glutathione transferase class log neg M96326_ma1_at HUMAZCDI azurocidin gene,
 log neg M96958_at HUMTDGF3A (clone CR-3) teratocarcinoma log neg
 M97796_s_at HUMID2X helix-loop-helix protein (Id- log neg M97815_at
 HUMCRABP02 retinoic acid-binding protein log neg S34389_at HMOX2 heme
 oxygenase-2 (human, kidne log neg S58544_at SPAG1 75 kda infertility-related
 spe log neg S69115_at S69115 granulocyte colony-stimulating log neg
 S69115_at S69115 granulocyte colony-stimulating log neg S71043_ma1_s_at
 S71043 Ig alpha 2=immunoglobulin A he log neg S71043_ma1_s_at S71043 Ig alpha
 2=immunoglobulin A he log neg S73591_at VDUP1 brain-expressed HHCPA78 homolo
 log neg S73591_at VDUP1 brain-expressed HHCPA78 homolo log neg S75463_at
 S75463 P43=mitochondrial elongation f log neg S77356_at S77356 transcript

ch21 =oligomycin sen log neg 577582_at S77582 HERVK10/HUMMTV reverse transcr
 log neg S78234_at S78234 nuc2 homolog [human, fibroblas log neg S78771_s_at
 S78771 NAT=CpG island-associated gene log neg 579219_s_at S79219
 metastasis-associated gene (hu log neg S79522_at S79522 ubiquitin carboxyl
 extension p log neg 580562_at CNN3 acidic calponin [human, kidney log neg
 582297_at S82297 beta 2-microglobulin (11bp del log neg S82597_ma1_s_at
 S82597 UDP-GalNAc:polypeptide log neg S90469_at POR cytochrome P450
 reductase [hum log neg U00947_s_at U00947 clone C4E 3.2 \(\CAC\)\n\(\GTG\)\ log
 neg U03397_s_at U03397 receptor protein 4-1BB mRNA, log neg U03398_at TNFSF9
 receptor 4-1BB ligand mRNA, log neg U04241_at U04241 homolog of Drosophila
 enhancer log neg U04313_at P15 maspin mRNA, :protease inhibi log neg
 U05340_at CDC20 p55CDC mRNA, :cell division c log neg U06155_s_at U06155
 chromosome iq subtelomeric seq log neg U06863_at U06863 follistatin-related
 protein pr log neg U06863_at U06863 follistatin-related protein pr log neg
 U09117_at PLCD1 phospholipase c delta 1 mRNA, log neg U09303_at EFNB1 T cell
 leukemia LERK-2 \(\EPLG2 log neg U09813_at ATP5G3 mitochondrial ATP synthase
 sub log neg U09953_at U09953 ribosomal protein L9 mRNA, :r log neg
 U10362_at U10362 GP36b glycoprotein mRNA, : log neg U10492_at HSMOX1 Mox1
 protein \(\MOX1\)\ mRNA, : log neg U12404_at U12404 Csa-19 mRNA, log neg
 U12404_at U12404 Csa-19 mRNA, log neg U12485_at U12465 ribosomal protein L35
 mRNA, log neg U12779_at U12779 MAP kinase activated protein k log neg
 U14391_at MYO1C myosin-1C mRNA, :myosin 1C log neg U14588_at PXN paxillin
 mRNA, :paxillin :pax log neg U14968_at U14968 ribosomal protein L27a mRNA,
 log neg U14969_at U14969 ribosomal protein L28 mRNA, : log neg U14970_at
 U14970 ribosomal protein 55 mRNA, :r log neg U14971_at U14971 ribosomal
 protein S9 mRNA, :r log neg U14971_at U14971 ribosomal protein S9 mRNA, :r
 log neg U14972_at U14972 ribosomal protein S10 mRNA, log neg U14973_at
 U14973 ribosomal protein S29 mRNA, : log neg U15177_at U15177 cosmid
 CRI-JC2015 at D108289 i log neg U16660_at ECH1 peroxisomal enoyl-CoA hydratase
 log neg U16799_s_at U16799 Na,K-ATPase beta-1 subunit mRN log neg U16861_at
 KCNJ2 inward rectifying potassium ch log neg U17077_at BENE BENE mRNA, :BENE
 protein log

US-PAT-NO: 6300473

DOCUMENT-IDENTIFIER: US 6300473 B1

TITLE: SLM-1: a novel Sam68-like mammalian protein

DATE-ISSUED: October 9, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Richard; Stephane	Montreal	N/A	N/A	CAX

US-CL-CURRENT: 530/350,530/324 ,530/352

ABSTRACT:

The present invention relates to two Sam68-like mammalian proteins, namely SLM-1 and SLM-2, and nucleic acid molecules encoding them. The invention also relates to expression vectors and cells capable of expressing the proteins and antibodies capable of specifically binding to the proteins. Kits for the assay of tyrosine kinase activity are discussed which may be used to determine whether or not a cell is cancerous. The present invention further relates to transgenic animals such as "knockout mice". Knockout mice may be used to study the effect of test compounds on SLM-1 or SLM-2 deficiency.

4 Claims, 0 Drawing figures

Exemplary Claim Number: 1

DATE FILED: June 29, 1999

----- KWIC -----

BSPR:

SLM-1 is a substrate for both tyrosine kinases and protein arginine methyltransferases and it has the property of binding many SH3 and SH2 domain containing proteins including Src kinases, Grb2, p120rasGAP and PLCg1. SLM-1 is a protein that is expressed ubiquitously in mammalian cells and functions as an RNA binding protein, binding poly U and poly A homopolymeric RNA.

BSPR:

SLM-2 is an RNA binding protein that shares the same signaling motifs as SLM-1 and Sam68. It is a substrate for both certain tyrosine kinases and protein arginine methyltransferases and it has the property of binding many SH3 and SH3 domain containing proteins. It binds poly G and poly A homopolymeric RNA. It is expressed mainly in the brain and skeletal muscle.

BSPR:

The biological activities of SLM-1 and SLM-2 include: (1) the property of serving as a substrate for one or more enzymes with tyrosine kinase activity, such as p60Src and p59fyn, (2) the property of serving as a substrate for enzymes with arginine methyltransferase activity, including such enzymes as protein arginine N-methyl transferases including PRMT1, PRMT2, and PRMT3, (3) the property of binding Src kinases, Src derivatives, or molecules with tyrosine kinase activity, e.g., when at least partially tyrosine phosphorylated, (4) the property of binding SH3 and SH2 domain containing proteins including Grb2, PLCg1, p120rasGAP and Grb2, e.g., when at least

partially tyrosine phosphorylated, and (5) the property of associating with RNA.

BSPR:

Cells from which SLM-1, SLM-2, SLM-1 derivatives, and SLM-2 derivatives may be isolated include both prokaryotic and eukaryotic cells. Preferred cellular sources for the isolation of SLM-1, SLM-2, SLM-1 derivatives, and SLM-2 derivatives include mammalian cells possessing high levels of tyrosine kinase and/or arginine methyltransferase activity. Of particular interest are mammalian cells transfected with tyrosine kinases such as Src, p59fyn, ZAP70, Syk, FAK, JAK and/or arginine methyltransferases such as PRMT1, PRMT2, and PRMT3. Other mammalian cell sources of interest for the purification of SLM-1, SLM-2, SLM-1 derivatives, and SLM-2 derivatives include mammalian cells stimulated by growth factors that bind to growth factor receptors that have tyrosine kinase or arginine methyltransferase activity. Another preferred source for preparations from which to purify SLM-1, SLM-2, SLM-1 derivatives, and SLM-2 derivatives is insect cells, preferably grown in tissue culture, and genetically modified by baculovirus expression vectors or the like to express SLM-1, SLM-2, SLM-1 derivatives, and SLM-2 derivatives and a tyrosine kinase and/or arginine methyltransferase. A particularly preferred source of SLM-1 and SLM-2 derivatives is the SF9 cell line. Another source can be obtained by producing recombinant SLM-1 and SLM-2 in bacteria or yeast as a fusion protein with tags such as histidine repeats or glutathione S-transferase proteins. It will be appreciated that purified SLM-1 and SLM-2 can be phosphorylated or methylated in vitro to yield purified methylated and/or phosphorylated SLM-1 or SLM-2.

BSPR:

Assays. The subject invention provides methods and reagents for performing assays capable of measuring the amount of tyrosine kinase and arginine methyltransferase activity present in a cell and the fraction of SLM-1 or SLM-2 molecules that are phosphorylated and/or methylated.

BSPR:

SLM-1, SLM-2, and their derivatives may be used as substrates for the detection and quantification of tyrosine kinase and arginine methyltransferase activity from a variety of cellular sources. It is desirable to measure tyrosine kinase or arginine methyltransferase activity for several reasons. Of particular interest is the measurement of tyrosine kinase or arginine methyltransferase activity produced by tyrosine kinases or arginine methyltransferase encoded by oncogenes and proto-oncogenes. Thus, assays for tyrosine kinase and/or arginine methyltransferase may be employed to determine whether a cell is cancerous or has cancer potential. Also of interest is the measurement of tyrosine kinase and/or arginine methyltransferase activity attributable to membrane bound ligand receptors with tyrosine kinase and/or arginine methyltransferase activity, since the extent of phosphorylation or methylation of SLM-1 or SLM-2 may be used to measure the extent to which ligands are binding to such receptors.

CLPR:

1. An isolated polypeptide comprising at least 25 consecutive amino acids of SEQ ID NO. 1, wherein the polypeptide contains at least 2 proline motifs, can act as a substrate for a tyrosine kinase, and can act as a substrate for

arginine methyltransferase.

CLPR:

3. A polypeptide encoded by a DNA comprising the nucleic acid sequence of SEQ ID NO. 3 wherein the polypeptide contains at least two proline motifs, can act as a substrate for a tyrosine kinase, and can act as a substrate for an arginine methyltransferase.

US-PAT-NO: 6239264

DOCUMENT-IDENTIFIER: US 6239264 B1

TITLE: Genomic DNA sequences of ashbya gossypii and uses thereof

DATE-ISSUED: May 29, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Philippson; Peter	Riehen	N/A	N/A	CHX
Pohlmann; Rainer	Lorrach	N/A	N/A	DEX
Steiner-Lange; Sabine	Bonn	N/A	N/A	DEX
Mohr; Christine	Allschwil	N/A	N/A	CHX
Wendland; Jurgen	Lorrach	N/A	N/A	DEX
Knechtle; Philipp	Oberwil	N/A	N/A	CHX
Rebischung; Corinne	Saint-Louis	N/A	N/A	FRX

US-CL-CURRENT: 536/23.1,435/320.1 ,536/24.3 ,536/24.32

ABSTRACT:

The present invention relates to the terminal sequencing of random genomic fragments performed with the filamentous fungus *A.gossypii*, to the sequences obtained therewith and the use of the sequences for forensic identification, to characterize genes and gene organization of this ascomycete by inter-genomic comparison, to identify biosynthetic genes that can be used as selection markers, to isolate promoters and terminators for application in a homologous as well as heterologous context, to find putative centromere containing clones, chromosome mapping, chromosome identifying, general information about chromosome organization and in addition to identify ORF containing SRS sequences with no homology to *S. cerevisiae* or any other organism which allows the identification of *A. gossypii* specific genes.

2 Claims, 0 Drawing figures

Exemplary Claim Number: 1

DATE FILED: December 24, 1997

----- KWIC -----

DETL:

has 1 identical to Zn(2)-Cys(6) fungal-type 1155,1470,1527,1535,1546,1595 binuclear cluster domain in the N-terminal region PAG1470UP YNR043w ERG19 Mevalonate kinase, generates mevalonate- 1 identical to 5-phosphate from mevalonate, needed for 1155,1470,1527,1535,1546,1595 ARS-CEN plasmid stability (regulation of autonomous replication) PAG1471RP YHR096c HXT5 Highly similar to hexose transporters HXT2 1 syntenie due to the transporter and HXT4 (*S. cerevisiae*) genes ; continued syntenie with plasmid PAG1469RP/UP PAG1471UP YHR094C HXT1 HEX1:Hexokinase II, converts hexoses to 1 chosen due to syntenie, the other hexose phosphates in glycolysis and plays a hits(YJL214W:HXT8;YDR345C; regulatory role in glucose repression YLR081W) had no higher sim. PAG1472RP YDR016c unknown function 1 weak case of syntenie PAG1472UP YDR014w hypothetical protein 2 weak syntenie PAG1473RP YMR097c has ATP/GTP-binding site motif 1 syntenie PAG1473UP YMR094w CTF13 kinetochore proteinCbf3, subunit c 1 syntenie; YMR096w: len 297aa, sim to YFL059p and

YNL333p.YMR095c: len 224aa, sim to YML334p PAG1474RP YOR070c unknown 1
 PAG1474UP YKR081c unknown 1 PAG1475RP 4 PAG1475UP YPR190c RPC82 RNA-POL III,
 third largest subunit 1 YGR049w Similar to Scm4p (SCM4_YEAST), 1 possible
 Cdc4p-interacting protein. PAG1476RP YML091c RPM2 Ribonuclease P of MT,
 generates mature 1 tRNA molecules by cleaving their 5' ends PAG1476UP
 YML126c HMGS 3-hydroxy-3-methylglutaryl coenzyme A 1 located near TUB3/YML124c
 synthase, functions in mevalonate synthesis PAG1477RP YER093c unknown
 function 1 syntenie YNL116w unknown 1 PAG1477UP YER091c MET6 Homocysteine
 methyltransferase, 1 syntenie.YER092w:len methionine synthase; 5-
 125:unknown methyltetrahydropteroyl triglutamate--
 homocysteinemethyltransferase- PAG1478RP YER022w SRB4 component of RNA-POLII
 holoenzyme and 1 syntenie Kornberg's mediator (SRB) subcomplex, required for
 basal transcription PAG1478UP YER021w SUN2 Component of 26S proteasome
 complex 1 syntenie PAG1479RP 4 PAG1479UP YJR091c JSN1 protein that when
 overexpressed can 1 almost all of the ORF on this suppress the hyperstable
 microtubule plasmid starting from codon 20 phenotype of tub2-150 PAG1480RP
 YMR167w MLH1 Mismatch repair protein and homolog of 1 syntenie; YMR168c:CBF3b,
 len E. coli MutL involved in repair of small 608aa YMR169c:ALD3, len
 insertions 506aa PAG1480UP YMR170c ALD2 Aldehyde dehydrogenase 1 syntenie
 PAG1482RP YLR214w FRE1 Ferric (and cupric) reductase, acts on ferric 1
 syntenie iron chelates external to the cell PAG1482UP YLR215c unknown
 function 1 syntenie PAG1483RP YDL171c GLT1 Glutamate synthase, involved with
 1 glutamine synthase in glutamate biosynthesis PAG1483UP YNR013c protein
 with sim to Pho87p and YJL198p, 1 member of the phosphate permease family,
 12 TMD PAG1484RP YNR006w VPS27 protein involved in vacuolar sorting 1
 PAG1484UP YPL256c CLN2 G1/S-specific cyclin, interacts with 1 CDC28p protein
 kinase to control the events at START PAG1485RP tRNA pre-tRNA-leu 1
 redundant PAG1485UP YGL170c with sim to phosphoribulokinase precursor 2
 (phosphopentokinase) PAG1486RP YNL161w SER/THR protein kinase of unknown 1
 function; related protein from N. crassa is required for hyphal elongation,
 has sim to DBF2, DBF20, YPK1, YPK2, and TPK2, strong sim to cAMP-dependent
 protein kinases like cot-1 and human myotonic dystrophy kinase MDK PAG1486UP
 YHR142w unknown function, has 7 potential TMD 1 PAG1487RP YOR036w PEP12
 PEP12:Syntaxin(t-SNARE) involved in 1 disturbed syntenie. Two genes Golgi to
 vacuole transport, len 288aa covered with RP-SRS YDR267C protein with sim to
 SEC13 and other 1 disturbed syntenie proteins with WD-40 repeats; has sim to
 transcription factors PAG1487UP YOR038c HIR2 HIR2:Histone transcription
 regulator, 1 disturbed syntenie required for periodic repression of 3 of the
 4 histone gene loci and for autogenous repression of HTA1-HTB1 locus by H2A
 and H2B PAG1488RP YIR007W YIB7 sim to endoglucanases 1 PAG1488UP YOL027C
 unknown,sim to YPR125p 1 PAG1489RP YBR001c NTH2 alpha,alpha-trehalase,
 converts alpha,alpha- 1 CEN- trehalose to glucose, promoter contains the
 PLASMID,HISTONES:SYNTE stress-regulated CCCCT-elements (STRE) NIE common to
 stress-induced genes, repressors: glucose PAG1489UP YBL003c HTA2 Histone H2a
 1 syntenie PAG1490RP YMR167w MLH1 mismatch repair protein and homolog of 1
 syntenie:YMR170c:ALD5.YMR E. coli MUTL 169c:ALD3 YMR168c:CBF3B PAG1490UP
 YMR170c ALD5 Aldehyde dehydrogenase 1 syntenie PAG1491RP 4 PAG1491UP YNL082w
 PMS1 protein required for mismatch repair, 2 homologous to MutL PAG1492RP
 YKR070w unknown function 1 two genes covered by RP-SRS YOR052c unknown
 function 1 two genes covered by RP-SRS PAG1492UP YLR292c SEC72
 SEC72:Component of ER protein- 1 translocation complex that includes
 SEC61,62,66 and KAR2p PAG1493RP YPL243w SRP68 signal recognition particle
 subunit 1 syntenie PAG1493UP YPL246c unknown function 1 syntenie.YPL245w:

has A(P- loop), len 454 YPL224c: len 339 PAG1494RP YOL095c HRE571 sim to S. aureus helicase pcrA 1 syntenie. YOL094c: RFC4: len 323 aa, replication factor C
 PAG1494UP YOL093w unknown function 1 syntenie. End of syntenie YJL007 unknown function 1 syntenie. End of syntenie PAG1495RP YGL227w with sim to Dictyostelium non-receptor 1 tyrosine kinase U32174; contains WW(WWP) domain of about 40aa which is also found in dystrophin, Rsp5p, and Ess1p PAG1495UP 4
 PAG1496RP YER020w GPA2 guanine nucleotide binding protein alpha 1 subunit involved in regulation of the cAMP pathway during mating PAG1496UP YJR109c CPA2 Carbamoylphosphat synthase, arginine 1 specific PAG1497RP YPL022w RAD1 component of the nucleotide excision 1 repairosome, homolog of human XPF xeroderma pigmentosum gene pRproduct and the mammalian ERCC-4 protein, required for double-strand-break induced recombination PAG1497UP YPL016w ADR6 SWI1; Component of the SWI/SNF global 1 end of gene covered by RP-SRS transcription activator complex, acts to assist gene-specific activators PAG1499RP YOR021c unknown function 1 PAG1499UP YPR133c unknown function 1 PAG1500RP YOL094c RFC4 replication factor c 1 PAG1500UP 4 PAG1501RP MITO- align DNA PAG1501UP MITO- align DNA PAG1502RP YLR056w ERG3 ERG3: C-5 sterol desaturase, an iron non- 1 syntenie; heme oxygen-required enzyme of the ergosterol biosynthesis pathway, ER retention signal PAG1502UP YPL055c SPT8 member of the TBP class of SPT proteins 1 syntenie that alter transcription start site selection, functionally relatet to SPT3p and TBP PAG1503RP YNL297c unknown 1 syntenie PAG1503UP YNL294c unknown, has 6 potential TMD 1 YPL296w: q-ORF, len 104. YPL295w: len 524, unknown PAG1504RP MITO- DNA PAG1504UP MITO- DNA PAG1505RP YOR007c sim to protein phosphatases 1 PAG1505UP YML002W unknown function 1 syntenie. Two genes covered on UP-SRS YML003w unknown protein 1 syntenie with YML002w PAG1506RP YLR454W unknown function 1 PAG1506UP 4 PAG1507RP YBR053c protein with sim to glucan-1,3-beta- 1 glucosidase PAG1507UP YDR028c SRN1 REG1: regulatory subunit for protein 1 phosphatase GLC7, required for glucose repression PAG1508RP 4 PAG1508UP YKL211c TRP3 Anthranilate synthase component II, first 1 useful as TRP-selectable marker and fourth steps in Tryptophan biosynthesis gene? pathway PAG1509RP YOR166c unknown function 1 PAG1509UP 4 PAG1510RP YGR056w unknown function, has high sim to 1 syntenie YLR357w PAG1510UP YGR057c unknown function 1 syntenie

US-PAT-NO: 6200782

DOCUMENT-IDENTIFIER: US 6200782 B1

TITLE: Construction of nucleoprotein based assemblies comprising addressable components for nanoscale assembly and nanoprocessors

DATE-ISSUED: March 13, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Smith; Steven S.	Los Angeles	CA	N/A	N/A

US-CL-CURRENT: 435/91.2,435/6

ABSTRACT:

A nucleoprotein based nanoprocessor is described. The nanoprocessor includes one or more chimeric fusion proteins linked to a DNA scaffold. Both components of the fusion protein are enzymes.

31 Claims, 8 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 10

DATE FILED: April 11, 1997

----- KWIC -----

DEPR:

Catabolite-gene Activator Protein (CAP) is a positive transcription factor from E. coli which activates transcription from promoters sensitive to catabolite repression. It acts as a dimer in the presence of cyclic AMP (cAMP) by binding to its DNA recognition sequence and inducing it to bend. The crystal structure of the bent-DNA has been obtained (22) and visual inspection of the 3-D model of the structure available from the Brookhaven protein database suggests that pro9 at the N-terminus could be used in a head to tail linkage placing a bacterial methyltransferase in front of the CAP protein without disrupting the capacity of the protein to interact with itself in the dimer or with its DNA recognition site.

US-PAT-NO: 6060250

DOCUMENT-IDENTIFIER: US 6060250 A

TITLE: Human transferases

DATE-ISSUED: May 9, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lal; Preeti	Santa Clara	CA	N/A	N/A
Bandman; Olga	Mountain View	CA	N/A	N/A
Hillman; Jennifer L.	Mountain View	CA	N/A	N/A
Guegler; Karl J.	Menlo Park	CA	N/A	N/A
Gorgone; Gina A.	Boulder Creek	CA	N/A	N/A
Corley; Neil C.	Mountain View	CA	N/A	N/A
Patterson; Chandra	Mountain View	CA	N/A	N/A

US-CL-CURRENT: 435/6,435/193 ,435/252.3 ,435/320.1 ,435/325 ,536/23.1 ,536/23.2

ABSTRACT:

The invention provides three human transferases (HUTRAN) and polynucleotides which identify and encode HUTRAN. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating or preventing disorders associated with expression of HUTRAN.

10 Claims, 7 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 7

DATE FILED: June 30, 1998

----- KWIC -----

BSPR:

Protein-arginine methyltransferases catalyze the posttranslational methylation of arginine residues in proteins, resulting in the mono- and dimethylation of arginine on the guanidino group. Known substrates are histones, heterogeneous nuclear ribonucleoproteins (hnRNPs), and myelin basic protein. This otherwise unusual posttranslational modification is common in hnRNPs and may regulate their function. hnRNPs function in the nucleus in mRNA processing, splicing, and transport into the cytoplasm. Homologous protein-arginine methyltransferases that methylate hnRNPs have been cloned from yeast, rat, and man. These protein-arginine methyltransferases contain five sequence motifs, termed region I, post-region I, region II, region III, and post-region III, that may be involved in binding S-adenosyl-methionine. One human gene (HRMT1L1) encodes a 433 amino acid protein. The other human gene (HRMT1L2) may be alternatively spliced to yield three protein-arginine methyltransferases, of length 343, 347, and 361 amino acids respectively, with different amino termini. The protein encoded by the cloned rat protein-arginine methyltransferase gene (PRMT1) interacts with the TIS21 protein and the homologous BTG1 protein. The intermediate-early TIS21 protein is the product of a gene induced by treatment of cells with mitogens such as

DRPR:

FIGS. 3A, 3B, and 3C show the amino acid sequence alignment between HUTRAN-3 (2525071; SEQ ID NO:3) and human arginine methyltransferase (GI 1808648; SEQ ID NO:32).

DEPR:

As shown in Table 2, each HUTRAN has been characterized with regard to its chemical and structural similarity with transferase molecules. As shown in FIGS. 1A and 1B, HUTRAN-1 and human glutamine-phenylpyruvate aminotransferase (GI 758591; SEQ ID NO:30) share 49% identity. As shown in FIGS. 2A and 2B, HUTRAN-2 and rat kynurenine/.alpha.-aminoadipate aminotransferase (GI 1050752; SEQ ID NO:31) share 71% identity. As shown in FIGS. 3A, 3B, and 3C, HUTRAN-3 and human arginine methyltransferase (GI 1808648; SEQ ID NO:32) share 27% identity.

DEPR:

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between HUTRAN-1 and glutamine-phenylpyruvate aminotransferase from man (GI 758591), between HUTRAN-2 and kynurenine/.alpha.-aminoadipate aminotransferase from rat (GI 1050752), and between HUTRAN-3 and arginine methyltransferase from man (GI 1808648). In addition, HUTRAN is expressed in cancerous, inflamed, male and female reproductive, nervous, and gastrointestinal tissues. Therefore, HUTRAN appears to play a role in autoimmune/inflammatory, neurological, reproductive, and gastrointestinal disorders, and cancer.

ORPL:

Abramovich, C. et al., "A protein-arginine methyltransferase binds the intracytoplasmic domain of the IFNAR1 chain in the type I interferon receptor", EMBO J., 16: 260-266 (1997).

ORPL:

Scott, H.S., et al., "Identification and Characterization of Two Putative Human Arginine Methyltransferases (HRMT1L1 and HRMT1L2)", Genomics, 48: 330-340 (1998).

US-PAT-NO: 6025194

DOCUMENT-IDENTIFIER: US 6025194 A

TITLE: Nucleic acid sequence of senescence associated gene

DATE-ISSUED: February 15, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Funk; Walter	Hayward	CA	N/A	N/A

US-CL-CURRENT: 435/320.1,435/325 ,536/23.1 ,536/23.5 ,536/24.1

ABSTRACT:

Human gene GC6 is expressed more abundantly in senescent cells than young cells. Isolated, purified, and recombinant nucleic acids and proteins corresponding to the human GC6 gene and its mRNA and protein products, as well as peptides and antibodies corresponding to the GC6 protein can be used to identify senescent cells, distinguish between senescent and young cells, identify agents that alter senescent gene expression generally and GC6 expression specifically; such agents as well as GC6 gene and gene products and products corresponding thereto can be used to prevent and treat diseases and conditions relating to cell senescence.

10 Claims, 0 Drawing figures

Exemplary Claim Number: 1,6

DATE FILED: November 19, 1997

----- KWIC -----

DETL:

R14113 27430 acidic fibroblast growth factor (FGF) R40903 28573 multidrug resistance protein 1 R13451 28375 opioid-binding cell adhesion molecule R14153 28513 topoisomerase 2 R14230 28422 neurofilament, subunit L R41176 29204 glycosyl phosphatidylinositol R15029 29363 neuromedin-B receptor R14703 30066 ankrin (integrin-linked kinase) R14937 30125 Vimentin R18500 30373 cell death suppression-interacting protein NIP3 R42752 31267 JNK2 R17189 32026 DNA-PK R17458 32432 cdk8 R44542 34005 pSK1 interferon gamma receptor accessory factor-1 (AF-1) R44553 33800 HSP70B R21092 36232 carbonic anhydrase I R34402 36987 ETS-related ergB R49611 37522 osteocalcin R50771 38829 Human mRNA for protein-tyrosine phosphatase R51032 38853 EGF receptor kinase substrate R54467 39602 steroid receptor TR2 R56618 41289 transcriptional regulator, via glucocorticoid receptor R59031 41138 FHF2 R59202 41480 MADS/MEF2 R66467 41882 Poly (ADP-ribose) polymerase R59620 42122 lysosomal membrane 85K sialoglycoprotein precursor R60862 42291 diacylglycerol kinase, gamma R60583 37855 onconeural ventral antigen 1 R59442 37827 tropomyosin-related protein, neuronal R59498 37836 retinoic acid receptor (RAR) X b R22815 130324 E-cadherin R23999 131137 perlecan R25994 132574 arachidonate 5-lipoxygenase R31984 134322 MU-type opioid receptor R32041 134451 wee1 R68531 137794 activin receptor isoform IIB2 R63093 138002 interferon b1 R53921 138209 laminin-related protein A3 R63470 138644 Cadherin 5 R62703 138797 VEGF-receptor R62940 139073 interleukin-2 receptor beta chain R64353 139288 5,10-methenyltetrahydrofolate synthetase R62384 139840

noradrenaline transporter R67970 140689 vitamin K-dependent gamma-carboxylase
 R63819 141321 grancalcin R71212 143014 bone morphogenetic protein-1 R77028
 144233 tumor necrosis factor receptor 2 related protein R79900 146042 inhibin
 beta A chain R79028 146213 cell death suppression-interacting protein NIP2
 R80217 147050 cyclooxygenase-2 (COX-2) R81583 147727 kappa-type opioid
 receptor H12306 148420 p21-activated protein kinase (Pak1) H12367 148425
 beta-globin R82176 148968 MAD-related gene SMAD7 H04544 150163 neuropeptide Y
 receptor Y1 H01810 150495 keratin, type I cytoskeletal 19 H01971 150638
 fibulin 1, isoform B H02312 151213 c-K-ras H03104 152206 RagA R50456 152778
 11-cis retinol dehydrogenase R50193 153195 human rad51 R48368 153826
 transforming protein RHOB R53012 154269 keratin, type I cytoskeletal 14
 R53185 154359 H-twist R55303 154790 low-affinity nerve growth factor receptor
 R72820 156180 lethal G protein-mutation suppressor, Gps1 R72827 156183 ICAM-3
 R72598 156272 p38 Beta (MAP kinase p38Beta) R73050 156431 CNTF receptor
 R73919 156753 E2F R72898 157881 ras-related GTPase, membrane associated, ARP1
 H26723 158231 N-acetylgalactosamine-6-sulfatase H24504 159795 plasma
 retinol-binding protein H24956 160664 proto-oncogene tyrosine-protein kinase
 receptor RET H25136 161038 inositol 1,4,5-triphosphate receptor (type 3)
 H25797 161569 presenilin 2 H27557 162772 early growth response protein 1
 H05603 43504 c-erbA (thyroid hormone receptor) H06322 44296 HPRT H11003 47359
 endothelin-1 H11603 47510 vesicle coat protein, neuron-specific H14704 48653
 transcription factor ETV1/ER81, ets-related H16591 49164 vascular cell
 adhesion protein 1 precursor H15590 49284 FHF3 H19129 50930 FGF homologous
 factor 1 (FHF 1) H24237 51940 beta-2-microglobulin precursor H29687 52854
 b-Catenin H14285 163644 early response protein NAK1 H22542 173707
 neuron-specific growth-associated protein / stathmin homolog H23818 173839
 PMS3 homolog mismatch repair protein H29847 174868 cysteine dioxygenase
 H40230 175266 heat shock protein, 75 kDa, mitochondrial H45381 176537 basic
 fibroblast growth factor (FGF) H40775 177310 ribosomal protein S9 H46925
 178048 estrogen receptor hSNF2b H46845 178308 neuronal pentraxin 1 (NPTX1)
 H51148 179603 RAB-3A R85117 180726 2',3'-cyclic nucleotide
 3'-phosphodiesterase H41908 182295 cytochrome P450 IIB6 H43131 182987
 keratin, type II cytoskeletal8 H43783 184238 MMP-like, disintegrin-like,
 cysteine-rich protein (MDC) H39991 186132 E-selectin R83789 186615
 GDP-dissociation inhibitor rho R83224 187147 ras inhibitor INX H37967 190593
 paraneoplastic encephalomyelitis antigen HUD (ELAV-like) H38240 191664
 thrombospondin 2 H39144 192435 TATA-binding protein (TBP) R89150 195614
 phenylalanine hydroxylase R89340 195702 ionizing radiation
 resistance-conferring protein R89340 195702 ionizing radiation
 resistance-conferring protein R95185 198775 erythropoietin receptor H82878
 198873 b-actin H48460 200579 laminin, M polypeptide (merosin heavy chain)
 R99791 200978 iron-responsive element-binding protein H48602 202057 Toll
 protein H48596 202058 lysosome-associated membrane glycoprotein 2 precursor
 H53585 202765 keratin, type II cytoskeletal7 H54347 203089 hepatoma-derived
 growth factor H60824 205239 protein kinase C theta H59352 206509 E2F2 R98050
 206795 asialoglycoprotein receptor 2 H60775 209153 fructose-bisphosphonate
 aldolase B H62035 209227 FGF receptor k-sam R39221 209283 Mitosis activating
 protein (MAP) kinase H69011 211285 sno oncogene H66704 211864 TNF receptor II
 associated protein (TRAF2) H69474 212414 retinoic acid receptor H85143 220177
 fructose-bisphosphonate aldolase C R50354 220419 LIF H91647 221076 Human mRNA
 for rod photoreceptor protein H91651 221092 nuclear respiratory factor 2 gamma
 subunit H92621 221653 neural cell adhesion and axonal path-finding molecule
 homolog H86642 223350 ceruloplasmin H79373 229335 insulin-like growth factor

II H92681 231542 neurofilament triplet M protein H73424 232622 23K highiy
 basic protein H74208 232714 protein BCL-2-alpha H72723 232772
 metallothionein-IIB H78484 233583 interleukin-1 receptor, type II H77454
 233684 RAB-8 H66259 234198 Cdk6 H79456 235135 integrin $\alpha 4$ H52673 235938 BAK
 H61204 236306 keratin, type I cytoskeletal 17 H80710 241484 B-myb H92970
 241993 HMG-CoA reductase H95081 243320 α -1 antitrypsin N39046 243508 rap-1B
 (ras related protein) N49908 243678 vitamin D3 binding protein N39202 243879
 Wilm's tumor gene N54791 244301 phospholipase A2 (Ca²⁺-sensitive) N54435
 244827 TGF-beta induced gene product (BIGH3) N53549 245490 cytochrome P450
 monooxygenase CYP2J2 N78068 248244 haptoglobin 1 N58777 248613 c-myb H83566
 249361 osteoclast stimulating factor H84388 249568 guanine nucleotide-binding
 protein rab5c-like protein H96326 250269 thiol-specific antioxidant protein
 H96451 251200 c-kit H96505 251421 BMP-4 receptor, type II H96519 251469 BMP-2
 receptor N26291 256842 ADP/ATP translocase N30606 257766 cyclin H N30878
 258129 trichohyalin N56778 258504 inhibin α N32142 258584 cAMP-responsive
 element modulator N56815 258589 C-REL proto-oncogene N29501 259291 integrin
 beta-5 N57463 259363 RAS-related protein RAB-9 N32784 259642 Human GTP
 cyclohydrolase I mRNA N42072 259927 5-lipoxygenase activating protein H99256
 260332 thrombospondin 4 H97938 260737 glucocorticoid receptor, α H99410
 262686 Mad homolog JV5-1 H99414 262691 glucocorticoid receptor, β N28416
 263688 Bfl-1, Bcl-2-related N20079 263732 ceramide glucosyltransferase N28551
 263940 helicase II (RAD54L) N20556 264074 IQGAP1 (ras GTPase activating-like
 protein) N20574 264099 tyrosinase N21349 265151 protein kinase,
 cAMP-dependent, catalytic, α subunit N20844 265267 heat shock 70 KD
 protein 1 N31113 265344 acid sphingomyelinase-like phosphodiesterase 3a,
 ASML3a N24967 267422 epidermal growth factor receptor HER3 N29996 268231
 calcineurin N26851 269647 erm, ets-related N24811 269753 p190-B, rho GAP
 Family N27159 269815 inhibin β A N42732 270927 guanine nucleotide-binding
 protein Rab5B N46403 273750 guanine nucleotide-binding protein Rab26 N38781
 273941 disintegrin-metalloprotease H49613 274134 carbonic anhydrase II R93351
 275610 thromboxane-A synthase N39219 276946 Ca²⁺/calmodulin-dependent protein
 kinase isoform gamma C N66100 278409 JNK activating kinase 1 W01322 278490
 RAS-like protein TC21 N62906 278638 bone inducing protein N48784 279435 ERK3
 N48796 279470 Mch3 N57553 279970 adenosine A2A receptor N48082 281778 TGF- β 2
 N51103 281981 protein kinase C μ N51472 282060 ERCC2(XP-D) N52079 282563
 CDK-activating kinase N53393 284031 transforming protein P21/N-RAS N52338
 284459 protein kinase C β II N62083 287500 scatter factor (HGF) N59150
 287687 interferon- α /beta receptor α chain N76623 289268
 calcium-binding protein S100E, EF-hand N59268 289600 lactotransferrin N77150
 289941 DNA alkylation damage repair protein ABH N90839 290366 neurofilament,
 66 kDa N62377 290563 prostaglandin G/H synthase 1 W02974 291350 P-cadherin
 W03390 291571 histamine N-methyltransferase W03485 291982 SMAD5 N68268 292326
 DNA primase 58 kDa subunit N91234 292477 MAX δ N63852 293111 uracil-DNA
 glycosylase 1 precursor N70358 295389 growth hormone receptor W05062 298676
 HSP27 N75376 298898 cardiac actin, α W15554 301138 phospholipase A2,
 membrane associated N89581 301449 vasopressin V2 receptor N89782 302071
 hevin, antiadhesive extracellular matrix protein-related N78944 302383
 α -N-acetylgalactosaminidase W19257, 302808, ??? W38564 302490
 G2/mitotic-specific cyclin B1 H41433 302484 protein kinase C ζ W38932
 304843 heme oxygenase 2 W38689 305014 ornithine decarboxylase W39150 305149
 IAP (inhibitor of apoptosis) N91919 306848 mineralocorticoid receptor

US-PAT-NO: 6017536

DOCUMENT-IDENTIFIER: US 6017536 A

TITLE: Simian immunodeficiency virus peptides with antifusogenic and antiviral activities

DATE-ISSUED: January 25, 2000

INVENTOR-INFORMATION:

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US-CL-CURRENT: 424/188.1,424/208.1 ,530/300 ,530/324 ,530/325 ,530/326

ABSTRACT:

The present invention relates to peptides which exhibit antifusogenic and antiviral activities. The peptides of the invention consist of a 16 to 39 amino acid region of a simian immunodeficiency virus (SIV) protein. These regions were identified through computer algorithms capable of recognizing the ALLMOTI5, 107.times.178.times.4, or PLZIP amino acid motifs. These motifs are associated with the antifusogenic and antiviral activities of the claimed peptides.

28 Claims, 50 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 62

DATE FILED: December 20, 1994

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DETB:

129-156 515-552 PBLAR.sub.-- STAAU REGULATORY PROTEIN BLAR1

STAPHYLOCOCCUS

AUREUS 87-114 122-161 234-261 281-312 503- 539 PBMP.sub.-- TREPA BASIC

MEMBRANE PROTEIN PRECURSOR TREPONEMA PALLIDUM 312-346 PBMR.sub.--

BACSU

MULTIDRUG RESISTANCE PROTEIN BACILLUS SUBTILIS 277-304 PBNZA.sub.-- PSEPU

BENZENE 1,2-DIOXYGENASE ALPHA SUBUNIT PSEUDOMONAS PUTIDA 36-63

PBNZB.sub.--

PSEPU BENZENE 1,2-DIOXYGENASE BETA SUBUNIT PSEUDOMONAS PUTIDA 119-153

PBNZD.sub.-- PSEPU P4 SUBUNIT PSEUDOMONAS PUTIDA 179-213 PBPS2.sub.-- DESAM

BPS2 PROTEIN DESULFUROLOBUS AMBIVALENS 157-237 242-290 311-355 391-425 543-

573 PBRAB.sub.-- PSEAE CARRIER PROTEIN PSEUDOMONAS AERUGINOSA 260-287

313-340

PBRAE.sub.-- PSEAE TRANSPORT PROTEIN BRAE PSEUDOMONAS AERUGINOSA

254-281

PBRAG.sub.-- PSEAE BRAG PROTEIN PSEUDOMONAS AERUGINOSA 7-34 PBTUB.sub.--

ECOLI

VITAMIN B12 RECEPTOR PRECURSOR ESCHERICHIA COLI 439-466 PBTUE.sub.-- ECOLI

VITAMIN B12 TRANSPORT PERIPLASMIC PROTEIN ESCHERICHIA COLI 6-33
 PBVGA.sub.--
 BORPE TRANSCRIPTION REGULATOR BVGA BORDETELLA PERTUSSIS 174-205
 BORDETELLA
 BRONCHISEPTICA PBVGB.sub.-- BORPE PERIPLASMIC PROTEIN BVGB PRECURSOR
 BORDETELLA PERTUSSIS 116-143 PBVGC.sub.-- BORPE SENSOR PROTEIN BVGC
 BORDETELLA PERTUSSIS 39-66 202-229 PBVGS.sub.-- BORBR VIRULENCE BVGS
 PROTEIN
 PRECURSOR BORDETELLA BRONCHISEPTICA 113-143 341-368 501-531 PBXA.sub.--
 CLOBO
 BOTULINUM NEUORTOXIN TYPE A PRECURSOR CLOSTRIDIUM BOTULINUM 313-340
 686-729
 733-762 815-842 851- 968- 1159- 893 995 1207 PBXB.sub.-- CLOBO BOTULINUM
 NEUORTOXIN TYPE B PRECURSOR CLOSTRIDIUM BOTULINUM 666-693 720-762 802-832
 853-
 1004- 1058- 890 1031 1089 PBXC1.sub.-- CLOBO BOTULINUM NEUROTOXIN TYPE C1
 PRECURSOR CLOSTRIDIUM BOTULINUM 86-113 314-341 730-773 798- 850- 825 892
 PBXD.sub.-- CLOBO BOTULINUM NEUROTOXIN TYPE D PRECURSOR CLOSTRIDIUM
 BOTULINUM
 473-500 526-576 727-770 804-831 847- 906- 1060- 892 963 1087 PBXE.sub.--
 CLOBO BOTULINUM NEUROTOXIN TYPE E PRECURSOR CLOSTRIDIUM BOTULINUM
 254-291
 350-381 704-753 773-811 890- 992- 1115- 917 1019 1149 PBXE.sub.-- CLOBU
 BOTULINUM NEUROTOXIN TYPE E PRECURSOR CLOSTRIDIUM BUTYRICUM 254-291
 350-381
 704-753 774-808 890- 992- 1115- 917 1019 1149 PBXF.sub.-- CLOBO BOTULINUM
 NEUROTOXIN TYPE F PRECURSOR CLOSTRIDIUM BOTULINUM 669-710 735-772 892-919
 1013- 1095- 1183- 1040 1122 1210 PC550.sub.-- MICAE CYTOCHROME C550
 MICROCYSTIS AERUGINOSA 3-30 PCADA.sub.-- BACFI PROBABLE
 CADMIUM-TRANSPORTING
 ATPASE BACILLUS FIRMUS 30-57 100-131 165-192 276-306 533- 567 PCADA.sub.--
 STAAU PROBABLE CADMIUM-TRANSPORTING ATPASE STAPHYLOCOCCUS AUREUS
 282-309
 536-570 PCADC.sub.-- ECOLI TRANSCRIPTIONAL ACTIVATOR CADC ESCHERICHIA COLI
 54-85 412-443 PCAFA.sub.-- YERPE F1 CAPSULE ANCHORING PROTEIN PRECURSOR
 YERSINIA PESTIS 203-240 416-457 530-557 619-646 PCAPA.sub.-- BACAN CAPA
 PROTEIN BACILLUS ANTHRACIS 108-138 PCAPB.sub.-- BACAN CAPB PROTEIN
 BACILLUS
 ANTHRACIS 36-70 PCAPP.sub.-- ANANI PHOSPHOENOLPYRUVATE CARBOXYLASE
 ANACYSTIS
 NIDULANS 248-293 PCAPP.sub.-- ANASP PHOSPHOENOLPYRUVATE CARBOXYLASE
 ANABAENA
 SP 98-125 157-184 687-728 PCAPP.sub.-- CORGL PHOSPHOENOLPYRUVATE
 CARBOXYLASE
 CORYNEBACTERIUM GLUTMICUM 15-42 PCAPP.sub.-- ECOLI
 PHOSPHOENOLPYRUVATE
 CARBOXYLASE ESCHERICHIA COLI 35-62 PCARA.sub.-- BACSU
 CARBAMOYL-PHOSPHATE
 SYNTHASE BACILLUS SUBTILIS 274-319 PCARB.sub.-- BACSU
 CARBAMOYL-PHOSPHATE
 SYNTHASE BACILLUS SUBTILIS 790-831 PCARB.sub.-- ECOLI CARBAMOYL-PHOSPHATE
 SYNTHASE LARGE CHAI ESCHERICHIA COLI 454-481 PCAT2.sub.-- STAAU
 CHLORAMPHENICOL ACETYLTRANSFERASE STAPHYLOCOCCUS AUREUS 7-34 87-114

PCAT3.sub.-- STAAU CHLORAMPHENICOL ACETYLTRANSFERASE STAPHYLOCOCCUS
 AUREUS
 7-34 87-114 PCATA.sub.-- ACICA CATECHOL 1,2-DIOXYGENASE ACINETOBACTER
 CALCOACETICUS 31-65 PCATA.sub.-- BACST PEROXIDASE/CATALASE BACILLUS
 STEAROTHERMOPHILUS 440-470 PCATA.sub.-- ECOLI CATALASE HPI ESCHERICHIA
 COLI
 579-606 PCATA.sub.-- MICLU CATALASE MICROCOCCUS LUTEUS 453-480 PCATA.sub.--
 SALTY CATALASE HPI SALMONELLA TYPHIMURIUM 515-542 580-607 PCATE.sub.--
 ECOLI
 CATALASE HP11 ESCHERICHIA COLI 175-202 PCAT.sub.-- CAMCO CHLORAMPHENICOL
 ACETYLTRANSFERASE CAMYLOBACTER COLI 84-111 PCAT.sub.-- CLOBU
 CHLORAMPHENICOL
 ACETYLTRANSFERASE CLOSTRIDIUM BUTYRICUM 88-115 PCAT.sub.-- ECOLI
 CHLORAMPHENICOL ACETYLTRANSFERASE ESCHERICHIA COLI 92-119 PCAT.sub.--
 PROMI
 CHLORAMPHENICOL ACETYLTRANSFERASE PROTEUS MIRABILIS 92-119 PCAT.sub.--
 STAIN CHLORAMPHENICOL ACETYLTRANSFERASE STAPHYLOCOCCUS INTERMEDIUS
 7-34
 87-114 PCAT.sub.-- STRAG CHLORAMPHENICOL ACETYLTRANSFERASE
 STREPTOCOCCUS
 AGALACTIVE 7-34 87-114 PCBHE.sub.-- COXBU CBHE PROTEIN COXIELLA BURNETII
 209-236 PCBPT.sub.-- THEVU CARBOXYPEPTIDASE T PRECURSOR
 THERMOACTINOMYCES
 VULGARIS 48-75 PCCA.sub.-- ECOLI TRNA NUCLEOTIDYLTRANSFERASE ESCHERICHIA
 COLI
 376-403 PCCMK.sub.-- SYN7 CO2 CONC MECH PROTEIN CCMK SYNECHOCOCCUS SP
 29-56
 PCCMM.sub.-- SYN7 CO2 CONC MECH PROTEIN CCMM SYNECHOCOCCUS SP 212-256
 331-372
 445-486 PCDAS.sub.-- THEET CYCLOMALTODEXTRINASE THERMOANAEROBACTER
 ETHANOLICUS
 305-332 PCDG1.sub.-- BACMA CYCLOMALTODEXT GLUCANOTRANS PRECURSOR
 BACILLUS
 MACERANS 439-466 616-643 PCDG2.sub.-- BACMA CYCLOMALTODEXT GLUCANOTRANS
 PRECURSOR BACILLUS MACERANS 210-251 436-466 615-642 PCDGT.sub.-- BACCI
 CYCLOMALTODEXT GLUCANOTRANS PRECURSOR BACILLUS CIRCULRANS 217-244
 442-472
 594-651 PCDGT.sub.-- BACLI CYCLOMALTODEXT GLUCANOTRANS PRECURSOR
 BACILLUS
 LICHENIFORMIS 217-244 442-472 594-647 PCDGT.sub.-- BACOH CYCLOMALTODEXT
 GLUCANOTRANS PRECURSOR BACILLUS OHBENSIS 430-471 PCDGT.sub.-- BACS0
 CYCLOMALTODEXT GLUCANOTRANS PRECURSOR BACILLUS SP 210-237 435-462
 615-642
 PCDGT.sub.-- BACS2 CYCLOMALTODEXT GLUCANOTRANS PRECURSOR BACILLUS SP
 409-471
 PCDGT.sub.-- BACS3 CYCLOMALTODEXT GLUCANOTRANS PRECURSOR BACILLUS SP
 210-237
 435-462 614-641 PCDGT.sub.-- BACSP CYCLOMALTODEXT GLUCANOTRANS
 PRECURSOR
 BACILLUS SP 210-237 435-465 615-642 PCDGT.sub.-- BACSS CYCLOMALTODEXT
 GLUCANOTRANS PRECURSOR BACILLUS SP 217-244 442-472 594-651 PCDGT.sub.--
 BACST
 CYCLOMALTODEXT GLUCANOTRANS PRECURSOR BACILLUS STEAROTHERMOPHILUS

586-646

PCDGT.sub.-- KLEPN CYCLOMALTODEXT GLUCANOTRANS PRECURSOR KLEBSIELLA PNEUMONIAE

212-239 PCEA1.sub.-- ECOLI COLICIN E1 PROTEIN ESCHERICHIA COLI 44-71 285-326

PCEA1.sub.-- SHISO COLICIN E1* PROTEIN SHIGELLA SONNEI 44-71 284-325 413-440

PCEA2.sub.-- ECOLI COLICIN E2 ESCHERICHIA COLI 334-368 PCEA3.sub.-- ECOLI COLICIN E3 ESCHERICHIA COLI 334-368 PCEA6.sub.-- ECOLI COLICIN E6 ESCHERICHIA COLI 334-368 PCEAB.sub.-- ECOLI COLICIN B ESCHERICHIA COLI 283-341

PCEAD.sub.-- ECOLI COLICIN D ESCHERICHIA COLI 284-311 PCEAM.sub.-- ECOLI COLICIN M ESCHERICHIA COLI 178-227 PCEAN.sub.-- ECOLI COLICIN N ESCHERICHIA COLI 119-146 173-200 PCEA.sub.-- CITFR COLICIN A CITROBACTER FREUNDII 228-258

PCEFD.sub.-- STRCL ISOPENICILLIN N EPIMERASE STREPTOMYCES CLAVULIGERUS 370-397

PCEIA.sub.-- ECOLI COLICIN IA PROTEIN ESCHERICHIA COLI 68-95 225-282 378-412

415-452 PCEIB.sub.-- ECOLI COLICIN IB PROTEIN ESCHERICHIA COLI 68-95 225-282

378-412 415-452 PCELA.sub.-- ACEXY UTP URIDYLYLTRANSFERASE ACETOBACTER XYLINUM

59-89 PCELA.sub.-- ECOLI PROTEIN CELA ESCHERICHIA COLI 76-103 PCFAA.sub.--

ECOLI CF A/I FIMBRIAL SUBUNIT A PRECURSOR ESCHERICHIA COLI 27-58

PCFAC.sub.--

ECOLI CF A/I FIMBRIAL SUBUNIT C PRECURSOR ESCHERICHIA COLI 138-187 388-456

561-595 PCFAD.sub.-- ECOLI CF A/I FIMBRIAL SUBUNIT D ESCHERICHIA COLI 133-160

PCFAE.sub.-- ECOLI CF A/I FIMBRIAL SUBUNIT E ESCHERICHIA COLI 180-207 244-271

PCH10.sub.-- ACYPS 10 KD CHAPERONIN ACYRTHOSIPHON PISUM SYMBIOTIC 57-95

BACTERIU PCH10.sub.-- BACSU 10 KD CHAPERONIN BACILLUS SUBTILIS 66-93

PCH10.sub.-- CHLTR 10 KD CHAPERONIN CHLOAMYDIA TRACHOMATIS 64-91

PCH10.sub.--

ECOLI 10 KD CHAPERONIN ESCHERICHIA COLI 57-84 PCH10.sub.-- HAEDU 10 KD

CHAPERONIN HAEMOPHILUS DUCREYI 68-95 PCH10.sub.-- LEGMI 10 KD CHAPERONIN

LEGIONELLA MICDADEI 57-84 PCH10.sub.-- RICTS 10 KD CHAPERONIN RICKETTSIA

TSUTSUGAMUSHI 65-92 PCH10.sub.-- THEP3 10 KD CHAPERONIN THERMOPHILIC

BACTERIUM

PS-3 66-93 PCH60.sub.-- ACYPS 60 KD CHAPERONIN ACYRTHOSIPHON PISUM

SYMBIOTIC

341-382 BACTERIU PCH60.sub.-- AGRTU 60 KD CHAPERONIN AGROBACTERIUM

TUMEFACIENS 117-163 339-370 425-466 PCH60.sub.-- AMOPS 60 KD CHAPERONIN

AMOEBIA PROTEUS SYMBIOTIC 299-333 BACTERIUM PCH60.sub.-- BACSU 60 KD

CHAPERONIN BACILLUS SUBTILIS 298-332 337-364 PCH60.sub.-- BORBU 60 KD

CHAPERONIN BORRELIA BURGDORFERI 125-163 299-358 PCH60.sub.-- BRUAB 60 KD

CHAPERONIN BRUCELLA ABORTUS 117-144 339-366 PCH60.sub.-- CHLPN 60 KD

CHAPERONIN CHLAMYDIA PNEUMONIAE 4-31 PCH60.sub.-- CHLTR 60 KD CHAPERONIN

CHLAMYDIA TRACHOMATIS 4-31 PCH60.sub.-- CHRVI 60 KD CHAPERONIN CHROMATIUM

VINOSUM 300-327 PCH60.sub.-- CLOAB 60 KD CHAPERONIN CLOSTRIDIUM

ACETOBUTYLICUM

238-332 337-364 455-482 PCH60.sub.-- CLOPE 60 KD CHAPERONIN CLOSTRIDIUM

PERFRINGENS 337-368 417-444 PCH60.sub.-- COXBU 60 KD CHAPERONIN COXIELLA

BURNETII 300-327 348-382 PCH60.sub.-- HAEDU 60 KD CHAPERONIN HAEMOPHILUS

DUCREYI 339-366 417-444 PCH60.sub.-- LEGMI 60 KD CHAPERONIN LEGIONELLA

MICDADEI 299-333 PCH60.sub.-- LEGPN 60 KD CHAPERONIN LEGIONELLA

PNEUMOPHILA

298-332 452-479 PCH60.sub.-- MYCLE 60 KD CHAPERONIN MYCOBACTERIUM LEPRAE

125-152 236-263 337-364 PCH60.sub.-- MYCTU 60 KD CHAPERONIN MYCOBACTERIUM

TUBERCULOSIS 125-152 337-364 & BOVIS PCH60.sub.-- PSEAE 60 KD CHAPERONIN

PSEUDOMONAS AERUGINOSA 339-366 PCH60.sub.-- RHILV 60 KD CHAPERONIN
 RHIZOBIUM
 LEGUMINOSARUM 117-163 322-370 425-466 PCH60.sub.-- RICTS 60 KD CHAPERONIN
 RICKETTSIA TSUTSUGAMUSHI 103-130 293-336 360-394 PCH60.sub.-- SYN7 60 KD
 CHAPERONIN SYNECHOCOCCUS SP 308-335 337-380 PCH60.sub.-- SYN3 60 KD
 CHAPERONIN SYNECHOCYSTIS SP 338-365 455-489 PCH60.sub.-- THEP3 60 KD
 CHAPERONIN THERMOPHILIC BACTERIUM PS-3 337-364 PCH62.sub.-- STRAL 60 KD
 CHAPERONIN 2 STREPTOMYCES ALBUS G 116-148 337-364 PCHB.sub.-- VIBHA
 N,N'-DIACETYLCITOBIASE PRECURSOR VIBRIO HARVEYI 21-48 772-799 PCHEA.sub.--
 BACSU CHEMOTAXIS PROTEIN CHEA BACILLUS SUBTILIS 373-400 590-617
 PCHEA.sub.--
 ECOLI CHEMOTAXIS PROTEIN CHEA ESCHERICHIA COLI 256-286 PCHEA.sub.-- SALTY
 CHEMOTAXIS PROTEIN CHEA SALMONELLA TYPHIMURIUM 162-197 PCHER.sub.--
 BACSU
 CHEMOTAXIS PROTEIN METHYLTRANSFERASE BACILLUS SUBTILIS 124-151
 PCHEW.sub.--
 ECOLI PURINE-BINDING CHEMOTAXIS PROTEIN ESCHERICHIA COLI 68-115
 PCHEW.sub.--
 SALTY PURINE-BINDING CHEMOTAXIS PROTEIN SALMONELLA TYPHIMURIUM 88-115
 PCHEY.sub.-- BACSU CHEMOTAXIS PROTEIN CHEY ESCHERICHIA COLI 22-49
 PCHEY.sub.-- SALTY CHEMOTAXIS PROTEIN CHEY SALMONELLA TYPHIMURIUM 22-49
 PCHI1.sub.-- BACCI CHITINASE A1 PRECURSOR BACILLUS CIRCULANS 491-518 566-593
 PCHIA.sub.-- ALTSO CHITINASE A PRECURSOR ALTEROMONAS SP 345-372 PCHIA.sub.--
 SERMA CHITINASE A PRECURSOR SERRATIA MARCESCENS 346-373 PCHID.sub.--
 BACCI
 CHITINASE D PRECURSOR BACILLUS CIRCULANS 102-161 189-216 PCHIT.sub.-- SACER
 CHITINASE SACCHAROPOLYSPORA ERYTHRAEA 92-119 PCHIT.sub.-- STRPL CHITINASE
 63
 PRECURSOR STREPTOMYCES PLICATUS

DETB:

PTRB1.sub.-- ECOLI TRAB PROTEIN ESCHERICHIA COLI 113-143 PTRBF.sub.-- ECOLI
 TRBF PROTEIN ESCHERICHIA COLI 12-39 PTRB1.sub.-- ECOLI TRBI PROTEIN
 ESCHERICHIA COLI 70-97 PTRC1.sub.-- ECOLI TRAC-1 PROTEIN ESCHERICHIA COLI
 1006- 1058 PTRC2.sub.-- ECOLI TRAC-2 PROTEIN ESCHERICHIA COLI 1102- 1149
 PTRC3.sub.-- ECOLI TRAC-3 PROTEIN ESCHERICHIA COLI 884-931 PTRD1.sub.-- ECOLI
 TRAD PROTEIN ESCHERICHIA COLI 297-348 PTREA.sub.-- ECOLI PERIPLASMIC
 TREHALASE
 PRECURSOR ESCHERICHIA COLI 362-403 477-508 PTREC.sub.-- ECOLI
 AMYLOTREHALSE
 ESCHERICHIA COLI 280-307 PTRFA.sub.-- ECOLI TRFA TRANSCRIPTIONAL REPRESSOR
 PROTEIN ESCHERICHIA COLI 5-32 105-132 PTRG1.sub.-- ECOLI TRAG PROTEIN
 ESCHERICHIA COLI 61-88 630-657 831-858 865-895 PTRG5.sub.-- ECOLI TRAG
 PROTEIN ESCHERICHIA COLI 196-223 PTRG6.sub.-- ECOLI TRAG PROTEIN
 ESCHERICHIA
 COLI 195-222 518-545 PTRI1.sub.-- ECOLI TRAI PROTEIN ESCHERICHIA COLI 155-209
 597-624 887-914 1350- 1377 PTRI2.sub.-- ECOLI TRAI PROTEIN ESCHERICHIA COLI
 155-209 597-624 887-914 1350- 1377 PTRI5.sub.-- ECOLI TRAI PROTEIN
 ESCHERICHIA COLI 47-74 328-371 PTRJ4.sub.-- ECOLI TRAJ PROTEIN ESCHERICHIA
 COLI 36-63 PTRM8.sub.-- ECOLI TRAM PROTEIN ESCHERICHIA COLI 5-32 PTRMA.sub.--
 ECOLI TRNA (URACIL-5-)-METHYLTRANSFERASE ESCHERICHIA COLI 107-137
 PTRMD.sub.-- ECOLI TRNA (GUANINE-N1)-METHYLTRANSFERASE ESCHERICHIA COLI
 115-142 226-253 PTRPA.sub.-- BACSU TRYPTOPHAN SYNTHASE ALPHA CHAIN BACILLUS

SUBTILIS 220-247 PTRPA.sub.-- CAUCR TRYPTOPHAN SYNTHASE ALPHA CHAIN
 CAULOBACTER CRESCENTUS 241-275 PRTPA.sub.-- PSEAE TRYPTOPHAN SYNTHASE
 ALPHA
 CHAIN PSEUDOMONAS AERUGINOSA 176-203 PTRPB.sub.-- ACICA TRYPTOPHAN
 SYNTHASE
 BETA CHAIN ACINETOBACTER CALCOACETICUS 79-113 PTRPB.sub.-- BACSU
 TRYPTOPHAN
 SYNTHASE BETA CHAIN BACILLUS SUBTILIS 76-103 318-345 PTRPB.sub.-- BRELA
 TRYPTOPHAN SYNTHASE BETA CHAIN BREVIBACTERIUM LACTOFERMENTUM 172-199
 PTRPB.sub.-- LACCA TRYPTOPHAN SYNTHASE BETA CHAIN LACTOBACILLUS CASEI
 83-117
 PTRPB.sub.-- LACLA TRYPTOPHAN SYNTHASE BETA CHAIN LACTOCOCCUS LACTIS
 77-104
 164-191 PTRPB.sub.-- VIBPA TRYPTOPHAN SYNTHASE BETA CHAIN VIBRIO
 PARAHAEMOLYTICUS 56-83 PTRPC.sub.-- BRELA INDOLE-3-GLYCEROL PHOSPHATE
 SYNTHASE BREVIBACTERIUM LACTOFERMENTUM 229-256 PTRPC.sub.-- ECOLI
 INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE ESCHERICHIA COLI 205-232
 PTRPC.sub.--
 LACLA INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE LACTOCOCCUS LACTIS 148-175
 PTRPC.sub.-- VIBPA INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE VIBRIO
 PARAHAEMOLYTICUS 346-376 PTRPD.sub.-- ACICA ANTHRANILATE
 PHOSPHORIBOSYLTRANSFERASE ACINETOBACTER CALCOACETICUS 223-250 260-294
 PTRPD.sub.-- PSEAE ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE
 PSEUDOMONAS
 AERUGINOSA 205-232 PTRPD.sub.-- PSEPU ANTHRANILATE
 PHOSPHORIBOSYLTRANSFERASE
 PSEUDOMONAS PUTIDA 205-232 PTRPD.sub.-- VIBPA ANTHRANILATE
 PHOSPHORIBOSYLTRANSFERASE VIBRIO PARAHAEMOLYTICUS 2-29 PTRPE.sub.--
 BACPU
 ANTHRANILATE SYNTHASE COMPONENT I BACILLUS PUMILUS 33-60 PTRPE.sub.--
 CLOTM
 ANTHRANILATE SYNTHASE COMPONENT I CLOSTRIDIUM THERMOCELLUM 165-226
 PTRPE.sub.-- LACLA ANTHRANILATE SYNTHASE COMPONENT I LACTOCOCCUS LACTIS
 142-191 PTRPE.sub.-- LEPBI ANTHRANILATE SYNTHASE COMPONENT I LEPTOSPIRA
 BIFLEXA 145-179 PTRPE.sub.-- RHIME ANTHRANILATE SYNTHASE RHIZOBIUM MELILOTI
 139-166 PTRPE.sub.-- SALTY ANTHRANILATE SYNTHASE COMPONENT I SALMONELLA
 TYPHIMURIUM 191-218 PTRPE.sub.-- SULSO ANTHRANILATE SYNTHASE COMPONENT I
 SULFOLOBUS SOLFATARICUS 143-183 298-328 PTRPE.sub.-- VIBPA ANTHRANILATE
 SYNTHASE COMPONENT I VIBRIO PARAHAEMOLYTICUS 9-36 54-81 PTRPG.sub.--
 ACICA
 ANTHRANILATE SYNTHASE COMPONENT II ACINETOBACTER CALCOACETICUS 12-39
 PTRPG.sub.-- AZOBR ANTHRANILATE SYNTHASE COMPONENT II AZOSPIRILLUM
 BRASILENSE
 4-31 PTRPG.sub.-- ECOLI ANTHRANILATE SYNTHASE COMPONENT II ESCHERICHIA
 COLI
 5-32 PTRPG.sub.-- LACLA ANTHRANILATE SYNTHASE COMPONENT II LACTOCOCCUS
 LACTIS
 4-31 PTRPG.sub.-- PSEAE ANTHRANILATE SYNTHASE COMPONENT II PSEUDOMONAS
 AERUGINOSA 12-39 PTRPG.sub.-- SALTY ANTHRANILATE SYNTHASE COMPONENT II
 SALMONELLA TYPHIMURIUM 5-32 PTRPG.sub.-- SERMA ANTHRANILATE SYNTHASE
 COMPONENT II SERRATIA MARCESCENS 9-43 PTRPG.sub.-- SHIDY ANTHRANILATE
 SYNTHASE
 COMPONENT II SHIGELLA DYSENTERIAE 5-32 PTRPO.sub.-- PSEAE PUTATIVE

TRANSCRIPTIONAL REGULATOR PSEUDOMONAS AERUGINOSA 147-174 PTRS2.sub.--
 ECOLI
 TRAS PROTEIN ESCHERICHIA COLI 85-119 PTRT3.sub.-- ECOLI RESISTANCE PROTEIN
 PRECURSOR ESCHERICHIA COLI 184-221 PTRY1.sub.-- SALTY TRAY PROTEIN
 SALMONELLA
 TYPHIMURIUM 30-57 PTRYP.sub.-- STRGR TRYPSIN PRECURSOR STREPTOMYCES
 GRISEUS
 80-107 PTSR.sub.-- STRAZ RRNA METHYLTRANSFERASE STREPTOMYCES AZUREUS
 126-153
 PTSST.sub.-- STAAU TOXIC SHOCK SYNDROME TOXIN-1 PRECURSOR
 STAPHYLOCOCCUS
 AUREUS 29-63 102-129 PTSX.sub.-- ECOLI CHANNEL-FORMING PROTEIN TSX
 PRECURSOR
 ESCHERICHIA COLI 225-252 PTTK.sub.-- ECOLI HYPOTHETICAL 24.3 KD PROTEIN
 ESCHERICHIA COLI 81-115 PTUS.sub.-- ECOLI SITE-BINDING PROTEIN ESCHERICHIA
 COLI 57-91 107-134 PTYCA.sub.-- BACBR TYROCIDINE SYNTHETASE I BACILLUS BREVIS
 117-147 534-561 1019- 1051 PTYF1.sub.-- TREPE ANTIGEN TYF1 TREPONEMA
 PERTENUE 106-143 PTYRA.sub.-- BACSU POSSIBLE PREPHENATE DEHYDROGENASE
 BACILLUS
 SUBTILIS 244-271 312-342 PTYRA.sub.-- ECOLI CHORISMATE MUTASE ESCHERICHIA
 COLI 3291-370 PTYRR.sub.-- ECOLI TRANSCRIPTIONAL REGULATORY PROTEIN TYRR
 ESCHERICHIA COLI 483-510 PTYSY.sub.-- LACCA THYMIDYLATE SYNTHASE
 LACTOBACILLUS
 CASEI 139-173 PTYSY.sub.-- LACLA THYMIDYLATE SYNTHASE LACTOCOCCUS LACTIS
 75-109 PTYSY.sub.-- STAAU THYMIDYLATE SYNTHASE STAPHYLOCOCCUS AUREUS
 69-96
 PUHPB.sub.-- ECOLI SENSOR PROTEIN UHPB ESCHERICHIA COLI 276-303 316-343
 PUHPB.sub.-- SALTY SENSOR PROTEIN UHPB SALMONELLA TYPHIMURIUM 276-303
 316-343
 PUMUC.sub.-- SALTY UMCU PROTEIN SALMONELLA TYPHIMURIUM 204-231 PUPP.sub.--
 ECOLI URACIL PHOSPHORIBOSYLTRANSFERASE ESCHERICHIA COLI 30-57
 PURAA.sub.--
 ECOLI URACIL PERMEASE ESCHERICHIA COLI 350-384 PURE1.sub.-- HELPY UREASE
 ALPHA
 SUBUNIT HELICOBACTER PYLORI 15-42 PURE1.sub.-- PROMI UREASE ALPHA SUBUNIT
 PROTEUS MIRABILIS 72-99 PURE1.sub.-- PROVU UREASE ALPHA SUBUNIT PROTEUS
 VULGARIS 72-99 PURE1.sub.-- UREUR UREASE ALPHA SUBUNIT UREAPLASMA
 UREALYTICUM
 13-40 483-517 PURE2.sub.-- HELPY UREASE BETA SUBUNIT HELICOBACTER PYLORI
 62-99 PURED.sub.-- HELPY UREASE OPERON URED PROTEIN HELICOBACTER PYLORI
 17-44
 PUREE.sub.-- PROMI UREASE ACCESSORY PROTEIN UREE PROTEUS MIRABILIS 57-84
 PUREF.sub.-- KLEAE UREASE ACCESSORY PROTEIN UREF PRECURSOR KLEBSIELLA
 AEROGENES 20-47 PUS45.sub.-- LACLA SECRETED 45 KD PROTEIN PRECURSOR
 LACTOCOCCUS LACTIS 44-98 150-223 276-303 PUSHA.sub.-- ECOLI P-SUGAR
 HYDROLASE
 PRECURSOR ESCHERICHIA COLI 56-83 PUSHA.sub.-- SALTY SILENT PROTEIN USHA(0)
 PRECURSOR SALMONELLA TYPHIMURIUM 56-83 PUVRA.sub.-- ECOLI EXCINUCLEASE
 ABC
 SUBUNIT A ESCHERICHIA COLI 527-554 871-898 PUVRA.sub.-- MICLU EXCINUCLEASE
 ABC SUBUNIT A MICROCOCCUS LUTEUS 579-606 619-646 684-718 922-949 PUVRA.sub.--
 PARDE EXCINUCLEASE ABC SUBUNIT A PARACOCCUS DENITRIFICANS 33-60
 PUVRC.sub.--

BACSU EXCINUCLEASE ABC SUBUNIT C BACILLUS SUBTILIS 342-372 511-538
 PUVRC.sub.-- ECOLI EXCINUCLEASE ABC SUBUNIT C ESCHERICHIA COLI 37-64 332-362
 PUVRD.sub.-- ECOLI HELICASE II ESCHERICHIA COLI 280-307 PVANA.sub.-- ENTFC
 VANCOMYCIN RESISTANCE PROTEIN VANA ENTEROCOCCUS FAECIUM 182-209
 PVANC.sub.--
 ENTGA VANCOMYCIN RESISTANCE PROTEIN VANC ENTEROCOCCUS GALLINARUM
 177-211
 PVIB4.sub.-- AGRT5 VIRB4 PROTEIN PRECURSOR AGROBACTERIUM TUMEFACIENS
 138-172
 PVIB6.sub.-- AGRT5 VIRB6 PROTEIN AGROBACTERIUM TUMEFACIENS 190-227
 PVIB6.sub.-- AGRT6 VIRB6 PROTEIN AGROBACTERIUM TUMEFACIENS 190-227
 PVIB6.sub.-- AGRT9 VIRB6 PROTEIN AGROBACTERIUM TUMEFACIENS 190-227
 PVIBX.sub.-- AGRT5 VIRB10 PROTEIN AGROBACTERIUM TUMEFACIENS 32-59 212-239
 PVIBX.sub.-- AGRT6 VIRB10 PROTEIN AGROBACTERIUM TUMEFACIENS 32-59 211-238
 PVIBX.sub.-- AGRT9 VIRB10 PROTEIN AGROBACTERIUM TUMEFACIENS 32-59 212-239
 PVIC1.sub.-- AGRRA VIRC1 PROTEIN AGROBACTERIUM RHIZOGENES 81-108
 TUMEFACIENS
 PVIC1.sub.-- AGRT5 VIRC1 PROTEIN AGROBACTERIUM TUMEFACIENS 81-108
 PVIC1.sub.--
 AGRT6 VIRC1 PROTEIN AGROBACTERIUM TUMEFACIENS 81-108 PVID3.sub.-- AGRRA
 VIRD3
 PROTEIN AGROBACTERIUM RHIZOGENES 149-176 265-292 PVIRA.sub.-- AGRT5 WIDE
 HOST
 RANGE (WHR) VIRA PROTEIN AGROBACTERIUM TUMEFACIENS 42-76 113-147 657-684
 PVIRA.sub.-- AGRT6 WIDE HOST RANGE (WHR) VIRA PROTEIN AGROBACTERIUM
 TUMEFACIENS 42-69 84-125 653-680 PVIRA.sub.-- AGRT9 WIDE HOST RANGE (WHR)
 VIRA PROTEIN AGROBACTERIUM TUMEFACIENS 42-69 84-125 653-680 PVIRB.sub.--
 SHIFL VIRB TRANSCRIPTIONAL ACTIVATOR SHIGELLA FLEXNERI 37-71 107-134 187-214
 252-291 PVIRF.sub.-- YEREN VIRULENCE REGULON TRANSACTIVATOR YERSINIA
 ENTEROCOLITICA 16-46 PVIRG.sub.-- AGRRA VIRG REGULATORY PROTEIN
 AGROBACTERIUM
 RHIZOGENES 34-61 PVIRL.sub.-- AGRT6 LIMITED HOST RANGE (LHR) VIRA PROTEIN
 AGROBACTERIUM TUMEFACIENS 106-157 PVISC.sub.-- ECOLI VISC PROTEIN
 ESCHERICHIA COLI 47-74 PVLPA.sub.-- MYCHR VARIANT SURFACE ANTIGEN A
 PRECURSOR
 MYCOPLASMA HYORHINIS 74-112 PVM03.sub.-- BORHE OUTER MEMBRANE
 LIPOPROTEIN 3
 PRECURSOR BORRELIA HERMSII 54-81 PVM07.sub.-- BORHE OUTER MEMBRANE
 LIPOPROTEIN 7 PRECURSOR BORRELIA HERMSII 332-359 PVM21.sub.-- BORHE OUTER
 MEMBRANE LIPOPROTEIN 21 PRECURSOR BORRELIA HERMSII 330-357 PVM24.sub.--
 BORHE
 OUTER MEMBRANE LIPOPROTEIN 24 PRECURSOR BORRELIA HERMSII 47-143
 PVM25.sub.--
 BORHE OUTER MEMBRANE LIPOPROTEIN 25 PRECURSOR BORRELIA HERMSII 315-356
 PVNFA.sub.-- AZOVI NITROGEN FIXATION PROTEIN VNFA AZOTOBACTER VINELANDII
 158-188 218-245 PVNFK.sub.-- AZOCH NITROGENASE VANADIUM-IRON PROTEIN
 AZOTOBACTER CHROOCOCCUM MCD I 68-95 PVNFK.sub.-- AZOVI NITROGENASE
 VANADIUM-IRON PROTEIN AZOTOBACTER VINELANDII 68-95 372-403 PVRP2.sub.--
 SALCH
 65 KD VIRULENCE PROTEIN SALMONELLA CHOLERAEE- SUIIS 509-536 PVRP2.sub.--
 SALDU
 65 KD VIRULENCE PROTEIN SALMONELLA DUBLIN 511-538 PVSDE.sub.-- SALDU
 VIRULENCE

PROTEIN VSDE SALMONELLA DUBLIN 3-36 PVHB.sub.-- VIBVU CYTOLYSIN SECRETION
PROTEIN VIBRIO VULNIFICUS 30-75

US-PAT-NO: 5859346

DOCUMENT-IDENTIFIER: US 5859346 A

TITLE: Crucifer AFT proteins and uses thereof

DATE-ISSUED: January 12, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Zhang; Hong	Boston	MA	N/A	N/A
Goodman; Howard M.	Newton Center	MA	N/A	N/A

US-CL-CURRENT: 800/298,435/320.1 ,435/419 ,530/370 ,536/23.6 ,800/301

ABSTRACT:

Purified DNA encoding crucifer AFT proteins and chimeric transcriptional activator proteins from such DNA are disclosed. Such proteins are also involved in plant defense mechanisms by interacting with proteins involved in protecting plants from pathogens. The recombinant polypeptides and fragments are useful in methods of modulating plant gene expression.

17 Claims, 18 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 13

DATE FILED: November 14, 1996

----- KWIC -----

BSPR:

We have identified and describe herein a novel plant transcriptional activator from the crucifer, *Arabidopsis thaliana*. In addition to its role as a transcriptional activator, we have also determined that this protein plays a role in plant defense mechanisms by interacting with proteins, e.g., 3-O-methyltransferase and ascorbate peroxidase, involved in protecting plants from pathogens. We named this protein AFT1 (*Arabidopsis* Fourteen-Three-three 1) because it shows sequence homology to the widespread 14-3-3 protein family.

US-PAT-NO: 5623054

DOCUMENT-IDENTIFIER: US 5623054 A

TITLE: Crucifer AFT proteins and uses thereof

DATE-ISSUED: April 22, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Zhang; Hong	Boston	MA	N/A	N/A
Goodman; Howard M.	Newton Center	MA	N/A	N/A

US-CL-CURRENT: 530/370,435/69.1 ,530/377

ABSTRACT:

Purified DNA encoding crucifer AFT proteins and chimeric transcriptional activator proteins from such DNA are disclosed. Such proteins are also involved in plant defense mechanisms by interacting with proteins involved in protecting plants from pathogens. The recombinant polypeptides and fragments are useful in methods of modulating plant gene expression.

6 Claims, 18 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 11

DATE FILED: June 23, 1994

----- KWIC -----

BSPR:

We have identified and describe herein a novel plant transcriptional activator from the crucifer, *Arabidopsis thaliana*. In addition to its role as a transcriptional activator, we have also determined that this protein plays a role in plant defense mechanisms by interacting with proteins, e.g., 3-O-methyltransferase and ascorbate peroxidase, involved in protecting plants from pathogens. We named this protein AFT1 (*Arabidopsis* Fourteen-Three-three 1) because it shows sequence homology to the widespread 14-3-3 protein family.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 09:34:12 ON 05 JUN 2002

=> fil .bec

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

0.21

0.21

FILES 'MEDLINE, SCISEARCH, LIFESCI, BIOTECHDS, BIOSIS, EMBASE, HCAPLUS, NTIS,
ESBIOBASE, BIOTECHNO, WPIDS' ENTERED AT 09:34:34 ON 05 JUN 2002
ALL COPYRIGHTS AND RESTRICTIONS APPLY. SEE HELP USAGETERMS FOR DETAILS.

11 FILES IN THE FILE LIST

=> s arginine methyltransferase#

FILE 'MEDLINE'

55530 ARGININE

13128 METHYLTRANSFERASE#

L1 73 ARGININE METHYLTRANSFERASE#
(ARGININE(W) METHYLTRANSFERASE#)

FILE 'SCISEARCH'

46303 ARGININE

9282 METHYLTRANSFERASE#

L2 82 ARGININE METHYLTRANSFERASE#
(ARGININE(W) METHYLTRANSFERASE#)

FILE 'LIFESCI'

13171 "ARGININE"

3731 METHYLTRANSFERASE#

L3 39 ARGININE METHYLTRANSFERASE#
("ARGININE" (W) METHYLTRANSFERASE#)

FILE 'BIOTECHDS'

1294 ARGININE

394 METHYLTRANSFERASE#

L4 1 ARGININE METHYLTRANSFERASE#
(ARGININE(W) METHYLTRANSFERASE#)

FILE 'BIOSIS'

65063 ARGININE

10052 METHYLTRANSFERASE#

L5 66 ARGININE METHYLTRANSFERASE#
(ARGININE(W) METHYLTRANSFERASE#)

FILE 'EMBASE'

49371 "ARGININE"

9873 METHYLTRANSFERASE#

L6 86 ARGININE METHYLTRANSFERASE#
("ARGININE" (W) METHYLTRANSFERASE#)

FILE 'HCAPLUS'

89659 ARGININE

12150 METHYLTRANSFERASE#

L7 109 ARGININE METHYLTRANSFERASE#
(ARGININE(W) METHYLTRANSFERASE#)

FILE 'NTIS'

289 ARGININE

43 METHYLTRANSFERASE#

L8 0 ARGININE METHYLTRANSFERASE#
(ARGININE(W) METHYLTRANSFERASE#)

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FILE 'ESBIOBASE'
    18090 ARGININE
    3101 METHYLTRANSFERASE#
L9      45 ARGININE METHYLTRANSFERASE#
        (ARGININE (W) METHYLTRANSFERASE#)

FILE 'BIOTECHNO'
    15354 ARGININE
    4436 METHYLTRANSFERASE#
L10     55 ARGININE METHYLTRANSFERASE#
        (ARGININE (W) METHYLTRANSFERASE#)

FILE 'WPIDS'
    4602 ARGININE
    245 METHYLTRANSFERASE#
L11     2 ARGININE METHYLTRANSFERASE#
        (ARGININE (W) METHYLTRANSFERASE#)

TOTAL FOR ALL FILES
L12     558 ARGININE METHYLTRANSFERASE#

=> s l12 and (gene/q or mouse or murine)
FILE 'MEDLINE'
    225818 MOUSE
    95757 MURINE
L13     52 L1 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'SCISEARCH'
    237783 MOUSE
    99081 MURINE
L14     52 L2 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'LIFESCI'
    90323 MOUSE
    43738 MURINE
L15     29 L3 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'BIOTECHDS'
    19898 MOUSE
    1423 MURINE
L16     1 L4 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'BIOSIS'
    625425 MOUSE
    128242 MURINE
L17     45 L5 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'EMBASE'
    487479 MOUSE
    88148 MURINE
L18     57 L6 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'HCAPLUS'
    260522 MOUSE
    87557 MURINE
L19     62 L7 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'NTIS'
    3765 MOUSE
    859 MURINE
L20     0 L8 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'ESBIOBASE'
    72747 MOUSE

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      32675 MURINE
L21      30 L9 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'BIOTECHNO'
      196717 MOUSE
      50610 MURINE
L22      40 L10 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'WPIDS'
      15972 MOUSE
      2448 MURINE
L23      1 L11 AND (GENE/Q OR MOUSE OR MURINE)

TOTAL FOR ALL FILES
L24      369 L12 AND (GENE/Q OR MOUSE OR MURINE)

=> s (steroid or glucocorticoid) (w)receptor#
FILE 'MEDLINE'
      68938 STEROID
      20883 GLUCOCORTICOID
      556515 RECEPTOR#
L25      9547 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'SCISEARCH'
      50321 STEROID
      21161 GLUCOCORTICOID
      577698 RECEPTOR#
L26      12501 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'LIFESCI'
      11037 STEROID
      5351 GLUCOCORTICOID
      185375 RECEPTOR#
L27      3043 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'BIOTECHDS'
      2086 STEROID
      226 GLUCOCORTICOID
      9724 RECEPTOR#
L28      143 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'BIOSIS'
      78508 STEROID
      24501 GLUCOCORTICOID
      651041 RECEPTOR#
L29      11414 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'EMBASE'
      84769 STEROID
      30944 GLUCOCORTICOID
      616325 RECEPTOR#
L30      11211 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'HCAPLUS'
      89761 STEROID
      23439 GLUCOCORTICOID
      562818 RECEPTOR#
L31      11724 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'NTIS'
      566 STEROID
      102 GLUCOCORTICOID
      5599 RECEPTOR#
L32      69 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

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FILE 'ESBIOBASE'
    16034 STEROID
    6165 GLUCOCORTICOID
    201989 RECEPTOR#
L33      3498 (STEROID OR GLUCOCORTICOID) (W)RECEPTOR#

FILE 'BIOTECHNO'
    17072 STEROID
    8340 GLUCOCORTICOID
    181238 RECEPTOR#
L34      4793 (STEROID OR GLUCOCORTICOID) (W)RECEPTOR#

FILE 'WPIDS'
    6781 STEROID
    884 GLUCOCORTICOID
    31314 RECEPTOR#
L35      258 (STEROID OR GLUCOCORTICOID) (W)RECEPTOR#

TOTAL FOR ALL FILES
L36      68201 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

=> s transcription?(10a)(activat? or coactivat?)
FILE 'MEDLINE'
    200179 TRANSCRIPTION?
    519340 ACTIVAT?
    2775 COACTIVAT?
L37      31017 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'SCISEARCH'
    170600 TRANSCRIPTION?
    599602 ACTIVAT?
    3675 COACTIVAT?
L38      34442 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'LIFESCI'
    91624 TRANSCRIPTION?
    180809 ACTIVAT?
    1578 COACTIVAT?
L39      20077 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'BIOTECHDS'
    10293 TRANSCRIPTION?
    17154 ACTIVAT?
    20 COACTIVAT?
L40      832 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'BIOSIS'
    202333 TRANSCRIPTION?
    580287 ACTIVAT?
    2861 COACTIVAT?
L41      34649 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'EMBASE'
    168850 TRANSCRIPTION?
    489996 ACTIVAT?
    2489 COACTIVAT?
L42      27392 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'HCAPLUS'
    218245 TRANSCRIPTION?
    982285 ACTIVAT?
    3324 COACTIVAT?
L43      42888 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

```

FILE 'NTIS'
2145 TRANSCRIPTION?
26928 ACTIVAT?
56 COACTIVAT?
L44 194 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'ESBIOBASE'
95107 TRANSCRIPTION?
202191 ACTIVAT?
1919 COACTIVAT?
L45 20120 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'BIOTECHNO'
139665 TRANSCRIPTION?
197166 ACTIVAT?
1573 COACTIVAT?
L46 22113 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'WPIDS'
9002 TRANSCRIPTION?
202518 ACTIVAT?
236 COACTIVAT?
L47 927 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

TOTAL FOR ALL FILES
L48 234651 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

=> s (l36 or l48) (10a)methyltransferase#

FILE 'MEDLINE'
13128 METHYLTRANSFERASE#
L49 24 (L25 OR L37) (10A)METHYLTRANSFERASE#

FILE 'SCISEARCH'
9282 METHYLTRANSFERASE#
L50 26 (L26 OR L38) (10A)METHYLTRANSFERASE#

FILE 'LIFESCI'
3731 METHYLTRANSFERASE#
L51 18 (L27 OR L39) (10A)METHYLTRANSFERASE#

FILE 'BIOTECHDS'
394 METHYLTRANSFERASE#
L52 0 (L28 OR L40) (10A)METHYLTRANSFERASE#

FILE 'BIOSIS'
10052 METHYLTRANSFERASE#
L53 30 (L29 OR L41) (10A)METHYLTRANSFERASE#

FILE 'EMBASE'
9873 METHYLTRANSFERASE#
L54 20 (L30 OR L42) (10A)METHYLTRANSFERASE#

FILE 'HCAPLUS'
12150 METHYLTRANSFERASE#
L55 43 (L31 OR L43) (10A)METHYLTRANSFERASE#

FILE 'NTIS'
43 METHYLTRANSFERASE#
L56 0 (L32 OR L44) (10A)METHYLTRANSFERASE#

FILE 'ESBIOBASE'
3101 METHYLTRANSFERASE#
L57 14 (L33 OR L45) (10A)METHYLTRANSFERASE#

```

FILE 'BIOTECHNO'
      4436 METHYLTRANSFERASE#
L58      11 (L34 OR L46) (10A)METHYLTRANSFERASE#

FILE 'WPIDS'
      245 METHYLTRANSFERASE#
L59      1 (L35 OR L47) (10A)METHYLTRANSFERASE#

TOTAL FOR ALL FILES
L60      187 (L36 OR L48) (10A) METHYLTRANSFERASE#

```

```

=> s (l24 or l60) and py=<1999 range=2001,
FILE 'MEDLINE'
'2001,' IS NOT A VALID RANGE FOR FILE 'MEDLINE'
SEARCH ENDED BY USER

```

```

FILE 'SCISEARCH'
      3666 PY=<1999
L61      0 (L14 OR L50) AND PY=<1999

```

```

FILE 'LIFESCI'
      7141 PY=<1999
L62      0 (L15 OR L51) AND PY=<1999

```

```

FILE 'BIOTECHDS'
      15 PY=<1999
      (PY=<1999)
L63      0 (L16 OR L52) AND PY=<1999

```

```

FILE 'BIOSIS'
      78502 PY=<1999
L64      0 (L17 OR L53) AND PY=<1999

```

```

FILE 'EMBASE'
      2062 PY=<1999
L65      0 (L18 OR L54) AND PY=<1999

```

```

FILE 'HCAPLUS'
      19894 PY=<1999
L66      0 (L19 OR L55) AND PY=<1999

```

```

FILE 'NTIS'
      15614 PY=<1999
L67      0 (L20 OR L56) AND PY=<1999

```

```

FILE 'ESBIOBASE'
      737 PY=<1999
L68      0 (L21 OR L57) AND PY=<1999

```

```

FILE 'BIOTECHNO'
      128554 PY=<1999
L69      22 (L22 OR L58) AND PY=<1999

```

```

FILE 'WPIDS'
      20247 PY=<1999
      (PY=<1999)
L70      0 (L23 OR L59) AND PY=<1999

```

```

TOTAL FOR ALL FILES
L71      22 (L24 OR L60) AND PY=<1999

```

```

=> fil medl
COST IN U.S. DOLLARS

```

```

SINCE FILE      TOTAL

```


	ENTRY	SESSION
FULL ESTIMATED COST	14.39	14.60

FILE 'MEDLINE' ENTERED AT 09:40:20 ON 05 JUN 2002

=> s (124 or 160) and py=<1999 range=2001000000,
93399 PY=<1999

L72 0 (L13 OR L49) AND PY=<1999

=> log y

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.38	14.98

FULL ESTIMATED COST

STN INTERNATIONAL LOGOFF AT 09:40:36 ON 05 JUN 2002